

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTACCAAGGCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGAAAAAATATTTAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTACAGCT
 TTGCTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACCTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACATATATTAGGGGGTCCCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTCGTCTTTGTGTCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAA**TG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAAATGGGGCAGATATGC
 ATTAAATAGTTTGTACAGCAGCTTTTCGTTGAAGTTAGAAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACTAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAAGCTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCATT
 GCTGAACCTTAACAAACTGTTTCATCCTGAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
 AATACAAACAGTATACTCATG

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGA

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

F0001-326869

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTTCGGTGGCGCCACGTCGCGCCCGTCTCCGCCCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCCGGGAGCCGGCCGCGTCTGAGGG
 GGTCCGCACGGGGAGTCCGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCCGAAG**ATG**TCGG
 ACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGGCCTATTGGTTCGCCGCCACCGTC
 CGCGTGCCTTTGGTCGGCAAACCTCGGCCCTCATCAGCCCGGCTACCTCTTCCTCTGGCCCGA
 AGCCTTCCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTTCTACGCCGA
 CTTGAACAGGAGCTTTTGTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
 TGTCACTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
 ACACGATTTAAGGCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCA
 GATACCCAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCTTCTGCTAGCATGAGCGCAGC
 TGCTGATCAGAATGGCGGAGGCCGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
 A**CTGA**AGGGGCGCGCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCCAGTCTCTGGGTG
 CACTTAACAACTCGCTTCTGGCTAACACTGTGGACCTGACCCACACTGAATGTAGTCTTTTC
 AGTACGAGACAAGTTTCTTAAATCCCCAAGAAATAAAGTTGTCCACAAGTTTCACGAT
 TCTCATTAAGTCTTACTGCTGTGAAGAACAATAACCACTGTGCAAAATGCAAACTGAC
 TACATTTTGGTCTCTCTCTCTCTCCCTTTCGCTCTGAATAATGGGTTTATAGGGGTCTCT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACCAACCTTCCCAAAGGACCTTATCTCTT
 TCTTGACACATGCTCTCTCCACTTTTCCCAACCCCACTTTTGAACACTAGAAAGTTG
 CCCATAAAATTTGCTCTGCCCTTGACAGGTTCTGTATTATTAGTCTTTTGCCAAGGCTGGTC
 ACAACAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTT
 AACCGTTTGGCACTCTTCAGATATTTTTTATAAAAAAAGTACCCTGAGTTCATGAGGGCCA
 CAGATTGGTTATTAATGAGATACAGGGTTGGTGCTGGGTGTTTTGTTCTGAGCTAAGTGA
 TCAAGACTCTAGTGGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGGGATGCACCCC
 TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
 ATTTCCCATTTCAATCTCATCTTGGATATGTGTTCAATGAGTAAAGGAGGAGAGACCCCTATA
 CGCTATTTAAATGTCACTTTCTTGCTATCCCCCGTTTTTTGGTCATGTTTCAATTAATTGT
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGGGTGTGTTA
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT
 TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA
 TGGCTTTGACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCAACCTTTGAGGCAACTAAAAAGGCTTCAAACGTTTGTATCAGTTTCTT
 TTCAGGAACATGTGTCTTAACAGTATGACTATTTCTTCCCCCATCTTAAACAGTGTGAT
 GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTATTTTGAATAGAGTTGTGTG
 TACTTCTCCATATTTAATTTATATGATAAAATAGTGGGGAGAGTCTGAACCTTAACTGTCA
 TGTTTTGTGTTGTTACCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACT
 CCAATTAATGTTGACGTACACTCATTTGTACAGGCGTGGAGACTCATTTGTATGTATAAGAATA
 TTTCTGACAGTGTGACCCGGAGTCTCTGGTGACCTCTACCACTCAGCTGCTGCTGCCGAG
 CAGTCATTTTTTCTAAAGGTTTACAAGTATTAGAAGCTTTTCAGTTTAGGGCAAATGTTTC
 ATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTTATGATTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGGACTTGACAAGGCCAAACA
 TGACAGTGGATTCTCTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTAAACTAATCCTTTTATTTGGTAAAAATGTAAATTAATAGTGAACCTT

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFR
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

000073-1000
FOREF-226660

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
 LVFDDEESKLTYTEIHQYEKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
 VLAAEDFTIFKAMMVQKNIEMLQAIIRIIQERNGVLPDCLTDGSDVVSLEHEEMKILREVL
 RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
 IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
 MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

1021-02555

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCCTTAGAAAATCAAAGAGGAATATGACCAGGAA

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CGCTGGTTTTGTTCTCAATAGCGGGCTTAGAGGGAGGGGCTTTTTGCCTATACCTTACT
TAGCTTCTCCACGATAGGCCCTTAAGGCTACTGCTGCTACTAGGGGCTAGACAGTTACTG
TCTCAGCTCTAGGATGTCGTTCTTCCCTAGAGCTCTCTGAGGGAGTATAAAAAC
AGTGGAAATGCGAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTGTCAACAATGTATAC
ATTCCTGCTAGGTGCCATATTTCATTGTTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
CTGCCAATGAGAAAAACAGTATGATTATCTTCCAACACTGCTGTAAGTGTGCTCGACAGCT
GTGAAGCTAGTTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
AAATTTGAAATATGCTTCTCGGAAGGAATTCTCTGATTTCATGAAGTGTCCATTCTGCCCT
TCTTTTATTTCTCGATAACTTGTATTGTTCTATGCTCTGCTATCTTCAACCGACGTCAT
GCTGTATTCTCTCAAAATTTAGACATTATAACACAGCTCTTCTATTAGGATAGTGTCTGAA
GAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACCTTTATTTTTGCTATTGTGGCCT
TGACTGCCGGGACATAAACTTTACAGCACAACCTTGCAGGACGTGGATTTCATCAGATGCTC
TTTTTCAGCCCTTCCAATTTCTGCTTCTTTTCAAGATGAGTGTCCCCAGAAAAGACAATTG
TACAGCAAAGGAATGGACTTTTCTGGAAGCTAAATGGAACACCCAGCCAGAGTTTTCAGTC
ACATCCGCTCTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTTCTTCAATGGGT
AATATCTATAATAAAAAGTACTGAAGGAGGGGACAGGCTACTGAAAGCATCTTCTATACA
GAACACGAACCTCTATTTCTTTGGCATTTCTGTTTTAATGGGCTGACTCTGGGCTCTCAGAGGA
GTAACCGTGATCAGATTAAAGAAGCTGTGGATTTTTTTATGGCCACAGTGGCATTTCAGTAGCC
CTTATTTTTGTAACTGCAATTCAGGCGCTTTCAGTGGCTTTTCATTCTGAAGTTCTGGATAA
CATGTTCCATGTCTTGATGGCCAGGTTACCACGTGCATTATACACACAGTGTCTGTCTGTG
TCTTTGACTTCAGGCGCTCCCTGGAATTTTTCTTGGAAAGCCCCATAGCCCTTCTCTATA
TTTTATTATAATGCCAGCAAGCTTCAAGTTCGGAATACGCACTGAGCAAGAAGGATCCG
AGATCTAAGTGGCAATCTTTGGGAGCGTCCAGTGGGGATGGAGAAGAAGCTAGAAGACTTA
CCAAACCCAAAGATGATGATCAGATGAGATACCTTTAACTGGTATCCCACTAGTTTGGCA
GCTCTCTGAACCTTATTTTTACATTTTCAGTGGTTGTAATATATATCTTTTCAATTTGATA
AACCAGAAATGTTTCTAAATCCTAATATTTCTTGATATATCTAGCTACTCCCTAAATGGTT
CCATCAAGGCTTAGATACCCAAAGGCTAAGAATTTCAAGAACTGATACGAGGAGTAAACA
ATATGAAGAATTCTAATAATCTCTAGTACTGTAATAATCAGAAAGTTATATGCGAGATTAT
TTTCTTGGCCTTCAAGCTTCCAAAAAAGTTGTAATAATCATGTTAGCTATAGCTTGTATAT
ACACATAGAGATTCAATTTGCCAAATATTCACATCATGTAGTTTCTAGTTTACATGCCAAAGT
CTTCCCTTTTTTAACTGTATAAAAGCTAGGTGTGCTCTGTAATTTTGAGGCCCTAGAGATAGT
CATTTTGCAAGTAAAGAGCAACGGGACCCTTTTAAAAACGTTGGTTGAAGGACCTAAATAC
CTGGCATACCATAGATTTGGGATGTAGTCTGTGCTAAATATTTTTGCTGAAGAAGCAGT
TTCTACAGCACAACATCTCAGATTTTAATTTTGAAATTCATGGGAATTTGATTTTGTG
TATATGCTTCTGTATGTTTTAAACATTTGGTTCCCTAGTCACCATAGTTACCACCTGTATTTTA
AGTCATTTAAACAAGCCACGTTGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTGAT
GTCAATACCTCTGACTTATACATTTTGAGATAAGAGGCACTTTTATTTTATAGTTAT
AATCTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAATGCTGGCTTCAGAATCATAC
CAGATTGTCAAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGATCCTTTTCAAAGGATCACTT
AGCAACACACATGTGACTTTTAACTGATGATGAATATTAATCTCTAAAAAGTAGAAGACC
AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCATGGTATTTTTCATG
GTATTTTGCATGCGAGCAGTTAATCTCTGTTAGATAGAGAAGTCAGGTGATAGATGATATTA
AAATTAGCAAAACAAAGTGACTTGTCTCAGGGTCATGCACTGGGTGATGATAGAAGAGTGGG
CTTAACTGGCAGGCTGTATGTTTACAGCATACCATAGTAATATAGACTTTATGTGTG
CATTTCTGAAAGATTTACATTTTCTGCTCTCTTTCTCCTAAGTTTCATGCGATGAATATA
AGGTAATATACTATTATATTAATTTGTGATATCCACAATAATATGACTGGCAAGAAATTG
GTGGAATTTGTAATTAATAATTAATAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
IFS NFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHD AFF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESD EDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGCGGGCTTAGAGGGAGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTGTCTATTGTGGCCTTGAAGCCGGA
CTAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTTGGGGGCGAGGAGCAT
 CCCGTCTACAGGTCCTAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGCGCCGAG
 AGCGGTCGCGGCGGGGCTGCTACCCACGAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
 CTATTGGATGTTGGCTCAGGTGGGCCCCCTTCTGCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGCAAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCGGTTCATTGCTACTTCTC
 ATCTGGTTCGTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATTGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGTGGGCAC
 AGTGCTGGGACGCGCATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTACAAAGTGCCAACCATACATGACATGGCACCCTTCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTATCCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCGAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTTCATGAGCCACGGCCCATACATCAAATCT
 ATTACTGGCTTCTCTTCACTTCCCTGGCTTTTCATGCTGGTGGAGGGAACTTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTTCATGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTCTCTTATGTCTTCTACCAAGTTTGCTCTGGAGTGTC
 ACTGGGCATTTTACCCTCAGTCTGGACTTTGACGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATGATGAGGAGAGGCGGCGGAGCAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCCCGACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGCTTGTCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACATTGCTGTGCTCACTGTGGGCGCGGCTGCTCTG
 TGGCCTCCTGCCTCCCCCTGCTGCTGCTGTGGGCGCAAGCCCTGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACATAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTATTTTCATAAAAGCTGGAAAGC

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCCG
 CAGTTTTATGCATTGCTACCATTATGTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTTCAGAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCCTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

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MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
 AAVLCIATIYVRYKQVHALSPEENVIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
 AVLTFMGMSLYMFVQTILSYQMOPKIHGKQVFIRLLLVICGVSALSMLTCSSVLHSGNFG
 TDLEQLKHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYRDFQKISLRVEANLHGLTLYD
 TAPCPINNERTRLLSRDI

FIGURE 16

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTGTTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGTCTGTCGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTCGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTTCTATTGTTTT
 TGAGACTTTTTCCCATGACACCAAACAGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCTATCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACATGATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCCCTCTAAAGCCCTCATTTGTTTGGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
IFGKQLVVSYFPDKVALLQRKVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCGATTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACGCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCTGGTGGACAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTCTGCC
 AACTGCACTGGCTGTGCCGAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFV
FTHLPFPKASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAACAGCTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGTCCTCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACCTGTCGCGACGCTGCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGGAAGTCC
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGCGCCACTTCATCGACAAACAGGTACAGCCAAC**CATG**TCCCAGTTTCGAAATG
 GACACGTATGCTAAGAGGCCACGACCTTATGTACAGTTTCTGGAATGCTCTGCTATGACATGCT
 TATGAGCAGTGGGCAGCGGCCAGTGGGAGCGCGCCAGAGTCTGCGGGCTTCCAGGAGC
 TGGTGCTGGAACCTGCCAGAGGCGGGCGCGCCTGGAGGGGCTACGCTACACGGCAGTGGT
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCTGGGCGCTGAGGACACTCCCATCCCCCGTGGAAACTGTCCA
 GCGCCGAGACATATTACGCATGCGCTCTGAAGTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC
 CTCACCTGCCCTTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCAGTTGCTGCAGG
 AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGAGACCCGATGGAGCGCAGCAGAATG
 GATGAGCAGCGTGAGGAAGCTGGTGCTGTGCGGCCAGTGGCAGCTGGTGACGGTAGTGGCCGT
 GGTCCCAGGGCTGCTGGAGGTACCACACAGAATGTATACTTTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCATCGGCTATGATTCCGGCGCCCACTGGCCAGCTGCGTGAG
 GTCCACCTGCGCGCTTTCAACCTGCGCCGTTACAGCACTTGAGCTCTTCTTTATCGATCAGGC
 CAACTACTTCTCACTTCCATGCAAGTGGGCACGACCCAGTCTCATCTCCTAGCCAGA
 CTCGAGACCCAGCCTGGCCCCATCCACCCCATACCCAGGTACGGGAACCAAGTTGTACTCG
 TGGCTCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGAT
 TGCTGCTGCCCTCAGGCCTTACCCAGAAATGGGTACAGCTGAGATATCCAACCTTCGAGTACT
 TGATGCAACTCAACACCATTCGCGGGCGGACCTACAATGACCTGTCTCAGTACCCTGTGTTT
 CCTGGGTCTGCAAGGACTACGTGTCCCCAACCTGGACCTCAGACCCACCGCTTCTCCG
 GGACCTGTCTAAGCCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT
 ATGAAGCTTTGAGGACCCAGCAGGGAACATTGACAAGTTCCACTATGGCAGCCCACTACTCC
 AATGCAAGCAGGCTGTGATGACTACCTCATCCGCGTGGAGCCCTTCACTCCTCGACAGTCCA
 GCTGCAAAAGTGGCGCTTTGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGCGCCTGGC
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTCTATTCTT
 GACTTCTTGGAGAACCAAGCAAGCTTTTGACCTGGCTGTCTCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTCTACGCCCTGGGGCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGCTGTGCACACCTACACGAGTGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGCGAGACTCCCTGTGAGCTGCTGAAGGAGCCACATCCAACCTCGGCTCTCA
 GCTGGAGGAAGCAGCCCATCGCCTTGCACGCTGGACACTAATCACTAGCATCTTCCAGCA
 CTTGAGCAACTCAAGGCTTCTTGCAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCACTACTTCACTTCAAGCAAGACCCC
 ACCATGGGCAGCCACAAGACGCGACCTGCTGAGTGGCCGTGGGTGCCAGGCAGTGGTGT
 GAGTGGAGCAAGCACTGGCAGTGGCCCCGATGGAAAGCTGCTATTACAGCGGTGGCCACTGGG
 ATGGCAGCTGCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCAGCTGCATGGTGTGGCGCTCCTGCATCAGGGTGGTGTGTGATGAGGCTGGCAC
 CAAAGCCTGTGCAAGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCAT
 GAACCTGACATGGCTGTGTCTGATCTGAGGATGGAATGTGATCATACACACTGTACGCCG
 CGGACAGTTTGTAGCGGCTCATCGGCCACTACGGCCTCTGGGTGCCACATCTCCTGGACCTATTTTCCACC
 TGGCATTGGGGTCCGAAGGCCAGATTGTGTTACAGAGCTCAGCGTGGGAACGTCCTGGGGCC
 CAGGTCACTACTCTTGGCACCTGTATTGACTCAATGGGAAGTTGCGGGCTTCACTGCCCCCT
 GGCAGAGCAGCTACAGCCCTGACGGTGACAGAGGACTTTGTGTGCTGGGCACCCGCCACT
 GCGCCCTGCACATCTCTCAACTAAACACACTGCTCCCGGCCCGCGCTCCTTGGCCCATGAAG
 GTGGCCATCCGCAAGCTGGCCGTGACCAAGGAGCGCAGCCACGCTGGTGGGCTGGAGGA
 TGGCAAGCTCATCGTGGTGGTCCGGGGGACCCCTCTGAGGTGCGCAGCAGCCAGTTTCGCGC
 GGAAGCTGTGGCGGTCTCTCGCGGCGCATCTCCAGGTGTCTCGGGAGAGACGGAATCAAC
 CCTACTGAGCGCGCTGA**GA**ACTTGCCAGTCCGGCTGCTCCGGCCCCCGCCCCCGGACGCCCTG
 GCCCGGGAGGCCCGCCAGAACTCGGCGGGGAACACCCCGGGTGGGAGCCAGCCAGGGGTGA
 GCGGGGCCACACCTGCCAGCTAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCCGCCCCCTCGCGGCTGAGGGGCGCGCTGAGGGCCAGCACTGGCGTCT

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FIGURE 23

MSQFEMDTYAKSHDMLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALELTP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSFQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSDRQFHSAVAAWQARLESPADVKEILP
 EFFEYFPDFLENQNGFDLGLCLQLTNEKVGDVVLPPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGSRDTCMVWRLRHQGGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGIQVQSSA
 WERPGAQVTYSILHLYSVNGKLRASLPLAEQPTALTVTDETVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGLKIVVAGQPSEVRSSQFARKLWRSRRISQVSS
 GETEYNPTFAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
TGGACCCTTAAGTGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTTGGAGCCCTCATCCTGACCCTTGTGCAG
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
TAAACCGAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTCTGGACAAAGTCACAGA
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGGTCTGTCTTCTTTT
TTTTCTCCGGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCCTGGGGCCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCTGGCCAACATGGTGAAACCTCC
GTCTCTATTAAAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
AAAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVGGVGVLSEFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLKILGKKN
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGTTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTCTGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCT
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGACAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGTGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTCGACGC
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCCGAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTGCGGGAAATGATTGAAGAGCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCATTTTGGGTTCAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCCCTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTTGTGTGTTTCGACAAAGAACC GGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCCTAGGAATTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPD EDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEED EHS GNDSDGSEPSEKRT RLEEEIVEQTMRRRQRREWEARRRDILF
DYEQY EYHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGV LQRH
VSRHNRHNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

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GTACCTCAGCGCAGCGCCAGGCGTCCGGCCCGCTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGATTCTGGGTGGCAAGAACTTAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAAAACACCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGGTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTCTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTCAGCTTTTAAACAATT
 GAGTAAAGTACGCTCCGGTCAACATGGTGTACAGCGCCCTGGGTCCCCTCTGGGCGACCGCTC
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCCCTGGATCCTGCCATGTATCCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCGCTGAGATCAGACCCATACATTATACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCAATGGGCCCTGCCAGGTACATGGGACGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCGTGCCAGAAGCGCTTCTTCGCTTCTCAGTGGGCGCAAGACGGCCCTGACACAGC
 GCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCGGCCAGTTTGTCTGCTCCCTGCGTGGCATCTACTTCTTACGCTCAATGTGC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCTATC
 CTGTACCGCAGCCCCAGCGAGCGCAGCATATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGG
 ACAGCTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTCAGGGG
 CCTCTGGGCCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCGCTCCCTGACAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCGGGGAGCTGGCATTCTGGGGAG
 CCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTCTTGTCTCTCTCTCTCTCT
 TGGACCTATTTTAAAGCTTGTCAACCTAAATATTCTAGAATTCTCCAGCTTCTGTATGCC
 AGCACTTCTCAAACCTTGAAATGCATGCGAATCACCCGGGTTCCGTGTTAAATGCAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCGTGTCTTCTCATATGTTCTCTGATGCTCTAG
 ATGGGGTCACTCTATGAACACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCCTCCCAACATTCTAGAAATCTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACATGC
 AACCTCTGCTCCCGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGCGCCTGCTACCATGCTGGCTAATTTTGTATTTTTAGTAGAGATGGGTTTACCATA
 TTGGCCAGGCTGCTTGAACCTCTGACTTCAGGTGACCAACCCGCTCGGCCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGCCACGCTGCCCTGGCCAATTTCAACATTTCTTAAATCTCTCAT
 CCTCCAGGGCTCCCGGTGCTATGTTCTCTTTACCCCTTCCCGCTTCTCTTGTCTCAGGGC
 TGCACCATGTCAGCCACCGTTTATTATTCATTATTAACACTGAGCACTGACTCTGTGCT
 GGGTCCCGGAAGGGTGAGGGGTGAGACACAGGCCCTGCCCTGCCCTCAGTACTGGCCA
 GTCCAGCCAGGCGGGGAGAGATGTGTACATAGGTTTAAAGCAGACCCAGAGCTCATGGGG
 GCTGTGTTCTGGGTGTTACAGTGTCTGCTGCTCCATTAACACTGCTCCCAAGGCTGG
 TGGGACGGGTCCCGGTGGCAGGGGCGAGTATCTCCTTCCCGTTCCTCATCCACCTGCCAG
 TGCTCATCTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCAGGAGTGTGGGGGCTTTGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGCATCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC
 CTTCTGCCCTCTCCACGGGCTCTGCCAGGGCTTGTCTAGTCCCTTCCACCAAAGTCTATCT
 GAATCTCCGTTTCCCCAGGGCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCTCATGCCCTCTCACCGGCCGACTGCCCGGACTCTCAGGCTTTATCAAGGTG
 CTAAGGCCGGGTGGGCGAGCTCCTCGTCTCAGAGCCCTCCTCCGGCTTGGTGTGCTCTTAC
 AAACACCTGCAGGAGAAGGCCCTCAGGAAAGCCCAAGGCTTAGAGCCCTCAGCAGGTCTGGG
 AGCTAGAGCAAGGAGGACCTCAGGCCCTCCGTTTCTTCTTCCAGGGTGGGGTGGCCTGGT
 GTTCCCCTAGCTTCCAAACCCAGGTGGCTGCCCTTCTCCCCAGAGGAGGCGGCTCCG
 CCATTGGTGTCTATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTGTCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCAGGA
 AGACCTGTGCTATAAACACCCCGCTGCTGATCTGCCCCTGCTGACCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGAATGCTGTCTCTTGGAAAAA

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPGQEGPGQSGKDGKMGMSPGAPCQKR
FAFSVGRKTAHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Signal peptide:

amino acids 1-20

amino acids 72-75

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCGCGGCCTCCCGGGACAGAAG**ATGT**G
 CTCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTTTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTCAC
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATCACCAATGAGACCTTCGGTGGCCTGCGGCGCT
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCCTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTACGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACGCGCCTGCGGCTGGCCGCAACAC
 CCGCATTGCCACAGCTGCGGGCCGAGGACCTGCGCGGCCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCTGCGG
 CTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTG
 GGTGCGCGAGAGCCACGTCACACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTGACTACGCCGACTTTGGCTGCCAGCCACCACC
 ACCACAGCCACAGTGCCCAACCAGAGGCGCGTGGTGCGGGAGCCACAGCCTTGCTCTTAG
 AGTACACGGTCAACAGCTGCGGCCAAGCCACTTACTCCGCTGTGTGTCATGCCTTTGGGG
 CCGGGGCGGGTGCCGGAGGGCGAGGAGGCTGCGGGGAGGGCCATACACCCAGCCGCTCCA
 CTCCAACCACGCCCCAGTCACCCAGGCCCGGAGGGCAACCTGCCGCTCCTCATTGCGCCCG
 CCTTGGCCGCGTGCTCCTTGGCCGCGCTGGCTGCGGTGGGGGACGCCCTACTGTGTGCGGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT
 GGAACCTGGAGGGAGTGAAGGTCCCTTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCACCGGGTCTGAGTGTGAGGTGCCACTCATGGGTTCCAGGGCTGGCCTC
 CAGTCAACCCCTCCACGCAAGGCCTACATC**TAA**GCCAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTGTGGTAACGCATGCCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA
 CCTTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGGAGCGGGTAGGCGGCTGTG
 TGACTCTAGTCTTTGGCCCGAGGAAGCGAAGGAACAAAGAAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGAAGACAACGATGATATG
 AAGGCCTTTTGTGAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDVTGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLEKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCPE
GFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPSTLRVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

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FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTATATGAGGAAATAAGTGGTAAAATCCTTGGAAATACA**ATG**AGACTCATCAG
 AAACATTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCCAGCCACAACGACACTGGATTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCTAGA
 TTTTCATTTCTGTCTCCAACTGAGAGTTTGTATCTATGCCATAACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG
 AAGAGTGTAACCTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTTGA
 GTGGGGCAAAAATACAAAATCAGATTCCAGAAAATGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTGAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC
 AAACTGCACATTTGTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGCGTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA
 ATGCAACGAAATCTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTAATAAGATGTA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAAATTTGTTGGCATACATCAGTGGAACTC
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTGTACTAC
 TCAAACTACTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTTCA
 ACAGGATAAAATCTATTTGCTTTTGGACAAAATGGACATAGAAAACCTGACAAATATAAATG
 CACAAATGCCACACATGCTTTTCCGAATTATCTACGAAATTTCAAATTTTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTTAAAGAAGTATCCAACCTGCCCTCACTTGAACACTCT
 CATTTTGAATGGCAATAAATCCAGACACTTTCTTTAGTAGTTGCTTTGCTAACACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGGCCAGAAACTGTGGTCAATATGAATCTGTCTATACAATAAAATTTGCTGATTTCTGCTCAG
 GTGCTTGGCCAAAAGTATTCAAATACTTGACCTAAATAACCAAACTCCAACTGTACCTTA
 AAGAGACTATTTCATCTGATGGCCTTACGAGAACTAAATATGCAATTTTAAATTTTCTAACTGAT
 CTCCTCGGATGCAGTCACTTTTCAGTAGACTTTTCAGTTCTGAACTTTGAAATGAACTTCATTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAAACTCTAAATGCGGGGAAGAA
 ATCCATTCGGGTGTACCTGTGGAATTAATAAAATTTCTTACAGCTTGAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTCTACACCTGTGAATACCCTTTAAACCTAAGGGGAAGTAG
 GTTAAAGACGTTTCATCTCCACGAATTAATCTTGCAACACAGCTCTGTTGATTGTCAACATTG
 TGGTTATTATGCTGCTTGGGTTGGCTGTGGCCTTCTGCTGCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAACCCA
 AGAACAACTCAAGAGAAATGTCGATTCACGCATTTATTTTCATACAGTGAACATGATTCTC
 TGTGGGTGAAGAAATGAATTTGATCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTGTC
 CTTTATGAAAGCTACTTTGACCTTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCAACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGCCCAACCAATCTCTTCCATGAAAATTTGATCATATAAATCTTTATC
 TTAAGTGAACCCATTCCATTTCTATTGCAATTTCCACCAGGTATCTAAACTGAAAGCTCTCTCT
 GGAAAAAAGCATACTTGAATGGCCCAAGGATAGGCTTAAATGTGGGCTTTTCTGGGCAA
 ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACAGAGAAATGTATGAAGTGCAGACA
 TTTACAGAGATTTAAATGAAGAGTCTCAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
ATAAAATCCCACAGTCTTGGGAAGTTGGGACCACATACACTTTGGGATGTACATTGATA
 CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAAGGTTATTTCCCTTCAATA
 TCAGTTTCTAGAAAGATTCTAGAAATGTATCTCTATAGAAACCTTCAACAAGTTTATAAGG
 GCTTATGAAAAAGGTTTCATCCAGGATTGTTTATAATCATGAAAAATGTGGCCAGGTTGC
 AGTGGCTCACTCTGTAAATCCCAGCACTATGGGAGGCCAAGTGGGTGAGCCACGAGGTCAA
 GAGATGGAGACCATCTGGCCAACTATGGTGAACCCCTGTCTCTACTAAAAATACAAAATTA
 GCTGGGCGTGATGGTGCACGCCCTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAAATCG
 CTTGAACCCGGAGGTGGCAGTTGTCAGTGAAGCTGAGATCGAGCCACTGCACTCCAGCCTGGT
 GACAGCGCAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAATGAAAAACATCTC
 TCATGGCCCAAAAATAAGGTCTAATTCATAAATTAATTAATTAATGTAATGTAATATAATTA
 CATGCCACTAAAAAGATAAAGTGAGCTGTATATTTCCCTGGTATGAAAAAACAATATAATAT
 GTTATAAATACTTAGTTGGTGGTGAAACCTAATTGTGGTTTTTGGCATTGAAATGGCATGAA
 ATAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTGGGCTGGGAGGTTGGA
 TTACAGGGAGCATTTGATTCTTCTATGTTGTGTATTTCTAATGATTTTGAATTTGTAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCTT

FIGURE 34

MRLIRNIYIFCSI VMTAEGDAPELPEERELMTNCSNM SLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHVSVKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENC SWPETVVNMNLSYNKLS
DSVFRCLPKSIQIIDLNNNIQTVPKETIHLMALRELNIAFNFLTDLPGC SHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKD VHLHELSCNTALLIVTIVVIMVLVLGLAVAFCC LHFDPWYLRMLGQCTQTWHRV
RKTQTQEQ LKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGGACCGGCCCTCGGAGGGGTGCGCGGGAAAGG
 GAGGGAAAGAAAGGCGGGGGCGGCCCCCTGCGCCCGCCCGCGCCCTGCGCGGCCCTGTCGCCGCCCTGTCGCCGCCGCG
 CCAGCCAGCCAGCCCGCGGGCGGCTCACACGCGCAGCCAGCGCGCCCTCCGCGGCCAAGCGCGCCGCT
 CTGCTGTGCCCTGCGCCCTTCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGCGCCCGCTGACCGTGA
 CCCTGCCCTGGGCGCGGGCGGAGCAGGCTGTCGCCCGCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC
 CTGGCAGTGACCTGGCGGGGTCGAGAGCCAGGGCGCAGCCCTCGAGGACCCCTGATTATTACGGGCAGGAGAT
 CTGGAGCCGGGAGCCCTACTACGCGCGCCCGAGGCCGAGCTCGAGACCTTCTCTCCGCGCTGCCTGCGGGCG
 CCGGGGAGGAGTGGGAGCGCGCCCGCAGGAGCCAGGCCGCCAAGAGGGGCCACCAAGCCCAAGAAAGCTCCC
 AAGAGGGAGAAGTCGGCTCGGAGCGCCCTCCACCAGGTAAACACAGCAACAAAAAGTTATGAGAACCAGAG
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAAGATGTGAGAGAGATTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAAATGAAAAATGATTTTATGACGGGACCGTGGTGCGCGGGAA
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGCGCCCTGACCAGATTCACTGGTGTATCACTCAAGGGA
 GGAATCCCTCTGGCTGAGTGACTGGTGACATCCTATAAGGTCACTGGTGAGCAATGACAGCCACAGTGGGT
 ACTGTTAAGAATGGATCTGGAGACATGATTATTGAGGGAAACAGTGAAGAAGGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCATGGTGGCCCGCTACATCCGCATAAACCCCTCAGTCTGGTTTGATAATGGGAGCATCTGCATGA
 GAATGGAGATCCTGGGCTGCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACAGAGATGACCACCCT
 GATGACCTGGATTAAAGCACCACAATTATAAGGAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCC
 CAATATCACCAGAATTACACAACTTGAAGAAAGCCACCGAGGCCCTGAAGCTGTATGGTGTGGAGATCTCAGATC
 ACCCTGGGGAGCATGAAGTCGGTGAGCCCGAGTTCACACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGC
 CGGGAGCTGCTGCTGCTGGTGGTGCAGTTCGTGTGTGACGAGTACTTGGCCCGGAATGCGGCATCTGTCCACT
 GGTGGAGGAGACCGGATTACGTCCCTCCCTCCCTCAACCCCGATGGCTACGAGAAGCCCTACGAAGGGGGCT
 CGGAGCTGGGAGGCTGGTCCCTGGGAGCGCTGGACCCACGATGGAATTGACATCAACAACACTTTCCTGATTTA
 AACACGCTGCTCTGGGAGGACAGGATCGACAGAATGTCCCGAGGAGGTTCCCAATCATATATTGCAATCCC
 TGAGTGGTTTCTGCGGAAATGCCACGGTGGCTGCCGAGACGAGAGCTCATAGCTGGATGGAAAAAATCC
 CTTTGTGCTGGGCGGCAACTGCAGGGCGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGGCGCTCCCC
 TGGAAAGCGCAGGAACACACCCCAACCCCGATGACCACTGTTCCGCTGGCTGGCTACTCCTATGCCTCCAC
 ACACCCCTCATGACAGACGCGCGGAGGAGGCTGCCACACGAGGACTTCCAGAAGGAGGAGGCACTGTCA
 ATGGGGCTCCTGGCACACCGTGCCTGGAAGTCTGAACGATTTCAGCTACCTTCATACAACTGCTTCGAAGT
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAACCGGGAATC
 TCTGATCGTGTTCATGGAGCAGGTTTCATCGTGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAAAGGAATCC
 CAAACGCCATTATCTCCGTAGAAGGCATTAAACATGACATCCGAACAGCCACGATGGGGATTACTGGCGCCTC
 CTGAACCTCGGAGAGTATGTGTCACAGCAAGGCCGAAGGTTTCACTGCATCCACCAGAAGCTGTATGGTTGG
 CTATGACATGGGGCCCAAGGTGTGACTTCACACTTAGCAAAACCAATGGCCAGGATCCGAGAGATCATGG
 AGAAGTTTGGGAAGCAGCCCGTCAAGCTGCCAGCCAGCGGCTGAAGCTGCGGGGGCGAAGAGACGACGAGCT
 GGGTGAACCTCCTGGGCCCTTGAGACTCGTCTGGGACCCATGCAAAATTAACCAACCTGGTAGTAGTCCATAG
 TGGACTCACTCACTGTTGTTTCCTCTGAATTCAAGAAGTGCTTGGGAAGAGGGTGCAATTGTGAGGCAGGTCC
 CAAAGGGAAGGCTGGAGGCTGAGGCTGTTTCTTTCTTGTGCCATTTATCCAAATAACTTGGACAGAGCA
 GCAGAGAAAAGTGTGGGAGTGAGAGACTCAGCAAGCCAACTGGGAATCAGAGAGAGAGGAGGAGGG
 GAGCTGTCCGTTGAGAGCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCTGTTTGGCTGGCAGCAAGG
 GTTCCACGTGCATTTGCAATTGACACAGCTAAATTCGAGCATTTCCCGAGCTGGGCTGTCCCAATGTTTACCA
 TTTGAGATGCTCCAGCGCTCCTAAGAGAATCCACCTCTCTGGCCCTGGAGCATTTGCAAGCTGTCAACAATAA
 ATTCTGTGTTCTTTTGACAATAGCGTCAATGCCAAGTGACATCAGTGAGCGCTCTTGAATCTGTTTAGTCTCCT
 TTTTCAACAAGGAGTGTGTTTCAGAAAAGGAGAGAGAGGCTGAGATCATTCAGGAGTTGTTGGGAGCAAGCA
 TGGAGCTCTTTGCACAAATCTGGGTCCATAAACACCCCAAGTCCTGCTGATCCAGTACGCCCTGGAGGT
 CCGCAGGTAGGAGAGCCAGCTGTCGACCTTCTGAAGGGCCAGAAAATTTAGCTGGATCTCCTCTTTTAC
 CTGCTAGGACTGGAAGAGCCAGAAAGTGGGGTGGCCTGAAGCCCTCTCTGCTTGGGATTGCCCCCTGTGTG
 GAATTGAGTGTCTATGGGTGGCCCTCATATCAGCCTGGGAGTATTTTTGATATGTAGAATGCCAGATCTTCCA
 GATTAGCTAAATGTAATGAAAACTTTAGGATTATCTGTGGAGCATCACTTTGGGAAGAAATTTTGAATT
 CTTGCAAGAAAAAGTATGTCACATTTTGTAAATGTTGCTGCCTCATTGACCTGGGAAAAATGAAAAA
 AATAAGCAAAATGGTAAGACCTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPP PGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR
LKLGRGRRRQRG

FIGURE 37

CTAAGAGGACAAAGATGAGGCCCGGCTCTCATTTCCTCTAGCCCTTCTGTTCTTCTTGGCCAAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCAGCCCCGGCTTCAGCTCTTTCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGCTCGGGCTCCAGCTCCAGCCGAGCTTACGAGCGGAGGTTCTGTGCCATTTGTT
 TTCCAATTTCCACCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCCTGTGTTCCCTGCCAGACACCACCTTTC
 CCGTGGACAGAGTGGAAACGTTGGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAAGTTTCTAA
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAAACTGTTAAACCTAACTGTCCGAATTGACATCAT
 GGAGAAGGATACCATTTCTTACACTGAAGTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTTGACCAGCTGGAGGTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCCTTGCCATTGCCCCAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTCTGCTCCACCTCTCCCACTC
 CAGGGAGCTGTGGTCATGGTGGTGGTGGTGAACATCAGCAACCCGCTCTGTGGTTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTTGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGTATGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTTGACCACCAACACGATTGCTGTGACTCAAACCTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTCATATGCTAATGTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTTATTCAACTGAAGCCAGCACTGGTAACATGGTGAATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCAACGCCCTTCATGGTATGTGGGGTCT
 GTATGCCACCGTACTATGAACACCAGAACAGAAAGAGATTTTTACTATTATGACACAACACAGGGGAAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTTGACCGAAAA
 CTTTATGCTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGAGAGCCCGAGTAAGCTGTTTA
 GAGGTTAGGGTGAAGAGAAAAATGTTGTTGAAAAATAGTCTTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAAGTGTGTTCAATTTTGAGCAATGTTTAGGTGCATAGTTCTACCACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTGCAATAAAGTCTGTCTAGGGTGGGA
 TTGTCAGAGGTCTAGGGGCACTGTGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAAGGAATTAACCTCAGTATGGCGCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC
 CTCATCCATGTAGCACCACTAATCTCTCCATGCCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAAATATCT
 GGAGCTCCTCGAGGGACCAATCTCCAACCTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGGTGCTGAGTTTTATGGAGAGAGGCCCTTTT
 ATGCAATTAATTTGACATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTCTTTTCTCTC
 ATTGTCCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCCCTCCAAGGCAGCTCAGAAGATTAG
 AACCGACTTACTAACCATTCCACCCCCACCAACCCCTTCTACTGCCTACTTTAAAAAATTAATAGTTTT
 CTATGGAAGTATCTAAGATTAGAAAAATTAATTTCTTTAATTTCATTATGAGACTTTAATTACATGACTCTA
 AGACTATAAGAAAATCTGATGGCAGTGACAAAGTGTAGCATTATTTGTTATCTAATAAAGACCTTGGAGCATA
 TGTGCACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCCCTTTGTTTAAAGCTGGAACCTGTAAGAAAT
 GAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAAAATAAATGAT
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSFSSSSRSGSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTCCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVISKPSVVQLNWRGFSYLYGAWGRDYSPQHHPNKGLYWVAPLNTDGRLLYYRLYNTLD
DLLLYINARELRITYGQGSGTAVYNNMYVNMNTGNIARVNLTNTIAVTQTLNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGLYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

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GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

TCTCGCAGATAGTAAATAATCTCGGAAAGCGCAGAAAGAGCTGTCTCCATCTTGTCTGTGAT
CCGCTGCTCTTTGTGACGTTTGTGGAGATCGGGGAGCGCTCTGGGGCTGTGCTCCATCGCGAGCT
GGATACCATGTGTTTGTGTGAAGATGCCCGTGTTTGCTATCCGATGCTGTCTAGTGGAAAC
AACTCCACGTGTAACTAGATGTATCATGCACTTTCTTGCTTGTGGATGTGTGTAGCTTG
TGTAATTGTTGATACCGGAATGGAAGAATCAAGTAAATAAGATCTCTGGATTTGTGGAAGT
AGAAAGGCTGTTGTCCCTTGTAACTATTTGGTGTGCTATAAAGCTGTATATCGTTTGTGCTTT
GGTTTGGCTATGTTCTATCTTCTTCTCTTCTTAACTAATGATCAAAGTAGAAGTAGACATGA
TCTTAGAGCTGCGAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTCGAGCAATTGCAATTA
TTATTTGGGCGATTTCTTATCCGAGAAGGAATCTTACACATGTGTGGTTTATGTAGGCAT
CGAGGTGCTTTTGTTCATCTTCATACCACTAGTCTTACTTATTTGTTTGTGACATTCATG
GAATGAATCGTGGGTTGAAAAATGGAAGAAGGAAGCTCGATGTGGTATGCGACGCTTGT
TATCAGCTACAGCTCTGAATATATCTGCTCTTTTAGTTGGTCTGCTCTGTTCTTGTCTAC
TACACTCATCCAGCGACTTGTTCAGAAACAAAGCGCTTCATCAGTGTCAACATGCTCTCTCTG
CGTTGGTCTTCTGTAAATGCTATCTGCCAAAATCCAGAATACCAACCAAGATCTGGTT
TGTTACAGTCTTCAGTAATACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
GAACCAAGAACAAATGCAACCCAGTCTACTAAGCATAAATGGCTACAAACCAACAGCAC
TGTCCTCAAGAAAGGCGAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTTATAGGACTAATTC
TCTTTTTGTGTGTGATTTTATTTACGACATCCGTCATTTCAACCAATGTCAGGTTATATAA
CTGACTCTAACAAAGTGATGAATCTACATTAATGAAGATGGTGGAGCTAGAAGTGATGATC
ACTGGAGATGGGGAGCAATGTTCACCCGAGCTAGATATAATGAAAGGATGGTGTCACTTACA
GTTATTCCTTCTTCTCACTTCATGCTTTTCTGGCTTCACTTATATCATGATGACCTTACC
AATCTGTCGAGGTATGAACCTCTCGTGAGATGAAAGTCAGTGGACAGCTGTCTGGGTGAA
AATCTCTTCAGTGTGATTTGGCATCTGTGCTGTATTTGGACATCTCGTGGCACCATTGTTC
TTACAAATCTGTGTTTGTGATCTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTTATGAC
TTATTTGAAAAACAGTATTTCCCAACTTTGTAAAGTTGTGTATGTTTGTCTCCCATGTAGC
TTCTCCAGTGTCTGCGATGAATTAGATTTTACTGCTTGTCAITTTGTTATTTTCTTACCAA
GTGCAATTGATATGTGAAGTAGAATGAATTCGACGAGGAAAGTTTATGAATATGGGTAGTGA
TAGTAAAAGTGGCCATTATTTGGGCTTATTTCTCTGCTCTATAGTTGTGAATGAAGAGTAAAA
ACAAATTTGTTTGACTATTTTAAATTTATAGCACTTAAAGTCTTTTATGAGCAATGATAAA
GCAAAATGATGGCTGCTTTTGAATATTTGATGTGTGGCTGGCAGGATCTGCAAGAAGAC
ATGGTTTATTTTAAATTTTATAAACAGTCACTTAAATGCGCAGTTGTCTTGAAATCTTTATA
AGGTTTACCCTTGATACCGGAATTTACACAGGTAGGAGTGGTTTAGTGCAATAGTGTAGG
TTATGATGGAGGTTGCTCGGTACTAAATTTGAATAACGAGTAAATATCTTACTTGGGTAGAGA
TGGCCTTTGCCAACAAAGTGAACGTTTGTGGTGTGTTTAAACCTAGTAGAATTTGGGTTGAGT
GGAAATGTTTGGAACTCTGAAGATTTAGACAAAGTTTGTGAAAAGGATAATCATGGGTTAGA
AGAAAGTGTGTTTGAAGTCACTTTGAAAGTATGATTTTGGGCCAGCAGGATGCTCACCCCT
GGTAATTTCCAGCAGCTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
GCTTGGCACAATGGTGAACCTGTTCTATAAAAAATATCTGCTTTGAGCATATGCTCTGTGGTC
CAGCAGCTGAGAGCTAGTGAAGATTTCTGACGCCACAGGCAAAGTTGCAGTGAAGCAAGTCA
CGTCACTGCACCTGAGCTGGGCACAGAGTAAAGCCAAAAAATATATATATTTGAATCAAGG
AGGCAAAATTTTGACAGGGGAAGGAAGTAACTGCAAAACCATAGGCTTTAGTAGGCTACTAT
ATAAAATCTAGTCCAGTTCTCTCATTTTAAAAAATGAAGACACTGAATATACAGACTTAAATA
GCTCAGATAGCTAATTTAGGAATTTCAAGTTGGCCAAATAAGCATCTCTCTGCATATTTAA
AAATAATTTCTATTCAAAATCATCGCAATTTGATTTACACCTCATAGTGTGATAATTTAATGT
GATGTGGATGCTGGTGTCCAGCATGACCCATAAACAGCTCAGAGAATGATGGAATGTGTTTT
AGATAAACTCCTGCTTATAGTATGACTACACAGTTCAAAGATGTTTAAATGCTCTTTGTAT
TTACTGCCATGTAATTTGAATTTATGATTTGCTAGTGTCTAATGAAGCTTTTAAATTCACAAAT
TCTCTTTTAAAAATTTTAAATGTGAATGGAATATAACAAATTCAGCTTAATTTCCCAACC
TTATTTCTGTGTGATAGACATTTGATTCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
ATGAATTCAGAGAAAAAATAAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTYLTWSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTYSSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSSWIGI
VLYVWTLVAPLVLTNRDFD

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FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCATNTTCTTCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC T
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTGTAACATTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA
AGATTCTCGATTTTTGTGAGAATGAGAAAGGTGTTGCCCTTGTAAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGCATTCTTCATTCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTCCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCTGCGATTGAGCTGCGGGTTCGCGGGCGCGCGGCTCTCCAAT
 GGCAAAATGTGTGGCTGGAGGCGAGCGGAGGCTTTCGGCAAAAGGCAGTCGAGTGTGTTGCGAGACCGGGGCGAG
 TCCTGTGAAAGCAGATAAAAGAAACATTTATTAACGTGTCTATTACGAGGGGAGCGGCCCGGGGCTGTCCG
 ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGCGAAAAGAGGCAGATTAC
 GTCGTTTCCAGCCAAAGTGGACCTGATCGATGGCCCTCTCTGAATTTATCAGATATTTGATTATTAGCGATTGCC
 CCCTGGTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC
 TGGGCGAATCCACATCTGTTTCAACTCTCCGCGGAGGGCGAGCAGGAGCGAGAGTGTGTGGAATCTGCGAGTG
 AAGAGGGACGAGGGAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACACAGAT
 CAGCAAAAAAGAAAGATGGGGCCCCCGAGCCTCGTGCTGTGCTTGTGTCCGCAACTGTGTTCTCCCTGTCTGGG
 TGGAGCTCGGCCTTCTGTGCGACACCAGCCTGAAAGGCAGGTTTACAGAGGACCGAGGAACATCCGCCCA
 ACATCATCTCGTGTCTGACGGACGACAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGCGC
 ATCATGGAGCAGGGCGGGGCGCACTTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCTCACGCTCCTC
 CATCCTCACTGGCAAGTACGTCACCAACCAACACCTACCAACAATGAGAAGTGTCTCGCCCTCTCTGGC
 AGGCACGACGAGAGCGCGCACTTTGCGCTGTACTCAATAGCATGGCTACCGGACAGCTTTCTTCGGGAAG
 TATCTTAATGAATACAACGCTCTCGACTGCCACCGGCTGGAAGAGTGGTGGGACTCCTTAAAAACTCCCG
 CTTTTATAACTACACGCTGTGTGGAACGGGGTGAAGAGAGACGCGCTCCGACTACTCCAAGGATTACCTCA
 CAGACCTCATCAACAAATGACAGCTGTGAGCTTCTTCCGACGCTCCAAAGAGATGTACCCGCGCAGTCTCTC
 ATGTGTCATCAGCCATGCGAGCCCCCAGGCTGAGGATTACGCCCAACAATATTCAGCCTCTTCCCAAACGC
 ATCTCAGACATACCGCGAGCTACAACCTACGCGCCCAACCCGAGCAACACCTGGATCATGCGCTACACGGGG
 CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTCGACGCGCTCATGTCTGGTGGAC
 GACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAAACAGTACATCGTATACACCGC
 CGACACCGGTTACCACATCGGCCGATTTGGCCTGGTGAAGGCGGCTGTCTGAATCCACATCGTCTCAACATTGACCTG
 TCCGTTTCTAGTGGGGGCCCAACGCTGGAAGCGGCTGTCTGAATCCACATCGTCTCAACATTGACCTG
 GCCCCACCATCTGGACATTTGACGGCTTGACATACCTGCGGATATGACGCGGAATCCATCTCAAGCTGCT
 GGACACGAGCGGCGGCTGGAATCGGTTTCACTTGAAGAAAGAGATGAGGCTCTGCGGGAGCTCTTCTGTGG
 AGAGAGCGCAAGCTGCTACACAGAGAGACAATGACAAGTGGACGCCGAGGAGGAGAACTTTCTGCCCAAGTAC
 ACGCGTGTGAAGACCTGTGTACGCTGTGAGTACCAGACGCGCTGTGAGCAGTGGGACAGAGTGGCAGTG
 TGTGGAGGACGCCACGGGAAGCTGAAGCTGCATAAGTGAAGGGCCCATGCGGCTGGGCGGACGACGAGCCC
 TCTCCAACCTCGTGCCCAAGTACTACGGGACGGGACGCGAGGCTGCACCTGTGACAGCGGGGACTACAAGCTC
 AGCCTGGCGGACGCGCGAAAAAATCTTCAAGAAGAAGTACAAGGCGAGCTATGTCCGCGCTCGCTCCATCCG
 CTCAGTGGCCATCGAGGTGGAACGCGAGGGTGTACCACGTAGGCTGGGTGATGCCGCCAGCGCCGAAACCTCA
 CCAAGCGCACTGGCCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGACTTCAGTGGCACTGGAGGCG
 CTTCCCGACTACTCAGCGCCCAACCCCTTAAAGTGCACATCGGTGCTACATCTAGAGAACGACACAGTCCA
 GTGTGACCTGGACCTGTCAAGTCTCTGACGCGCTGAAAGACCAAGCTGCACATGCACACAGAGATTTGAAA
 CCTCGCAGAACAAATTAAGAACCTGAGGGAAGTCCGAGGTCACTTGAAGAAAGCGGCCAGAGAATGTGAC
 GTGCACAAATCAGCTACCAACCCAGCACAAAGGCGGCTCAAGCACAGAGGCTCCAGTCTGCATCTTTTCAG
 GAAAGGCTGCAAGAGAAAGCAAGGTGTGGCTGTTGCGGGAGCAGAAAGCGCAAGAAAGAACTCCGCAAGCTGC
 TCAAGCGCTGCAAGAACACGACAGTGCAGCATGCCAGGCTCACGTGCTTACCCACGCAACACGCACTGG
 CAGACGGCGCCTTTCTGGACACTGGGGCTTTCTGTGCTGCAACGCGCCAAACATAACACGTACTGGTGCAT
 GAGGACCATCAATGAGACTCAAAATTTCTCTTCTGTGAATTTGCAACTGGCTTCTTACAGTACTTTGATCTCA
 ACACAGACCCCTACAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCTTCAACGACTACAGCTACAG
 CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGGACCTGGATGGAG
 AAGCTATGAGCAATACAGGCACTTTTCAGCGCTGAAAGTGGCCAGAAATGAAGAGACCTTCTTCAAAATCACTGG
 GACAACTGTGGGAAGGCTGGGAAGTTTAAAGAAACACAGAGGTGGACCTCCAAAAACATAGAGGATCACTGA
 CTGCACAGCAATGAAAACCATGTGGGTGATTTCAGCAGACCTGTGCTATTGGCCAGGAGGCTGAGAAAGC
 AAGCAGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACGACGAGGAGCAAGATTAACCTCAGGAAGTCC
 ATTTTTGCCCTGCTTTTGTGTTGGATTATACCTCACCAGCTGCACAAATGCAATTTTCTGTATCAAAAGTCC
 ACCACTAACCCCTCCCCAGAGCTCACAAAGGAAACGGAGAGAGCGAGCGAGAGAGATTCTCTGGAAATTTT
 TCCCAAGGCGAAAGCTCATTTGGAATTTTAAATCATAGGGGAAAGCGAGTCTGTCTTAATCTCTTATTCTT
 TGTGTTTGTCAAAAGAGGAACTAAGAACGAGGACAGAGGCAACGTGGAGAGGCTGAAACAGGTGACGAGACG
 TTTGACAATGAGTCAGTAGCAAAAGAGATGACATTTACCTAGCACTGAACACCTGTTTGCCTCTGAAGAAA
 CTGCCCTTCAATGTATATATGTGACTATTACATGTAATCAACATGGGAACCTTTAGGGGAACCTATAAGAAAT
 CCAATTTTCAGGAGTGGTGGTGTCAATAACGCTCTGTGCCAGTGTAAAGAAAAA

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FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIILVLTDDQDVELGSMQ
 VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGYVHNHNTYTNNENCSSPSWQAQHE
 RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
 YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP
 SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQTLMSVDDSMETIYNMLVETGELDNT
 YIVYTADHGYHIGQFGLVGKKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
 AGLDIPADM DGK SILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
 FLPKYQRVKDL CQRAEYQTACEQLGQKWQVEDATGKLLKHKCKGPMRLGGSRALSNLVPKY
 YGQGSEACTCD SGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ
 PRNLTKRHWPGAPEDQDDKDG GDFSGTGGLPDYSAANPIKVTHRCYILENDTVQC DL DLYKS
 LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGR LKHRGSSL
 HPFRKGLQE KDKVWLLREQKRKKKLRKLLKRLQNN DTC S MPGLTCFTHDNQHWQTAPFWTLG
 PFC ACTSANNNTYWC MRTINETHN FL FCE FATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
 HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRFPSSKSLGQLWEGWEG

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FIGURE 48

AACAAAGTTCACTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTTGAGGCTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGACAGTACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQWPWPF
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCC**ATGT**CGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTACACCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGGGCAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGAGAGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAAGTTGCTGAGGAAGTGCAGAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTTGC
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTTGTGTCTTTTTTTCAGACTC
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCACVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPAR
QGDFFYPPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAAC**T**ACTGGCTAAAGCTGGTGAAGGGCATT**T**TGCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCAT**T**GGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

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FIGURE 54

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCCAGTCATGACCCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCAC TAATCCGAGCCAAC TACTGGCTAAAGCTGGTGAAGGGCATTTTGCCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAAGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAA ACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACCGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

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FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGCTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCAACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGCCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAACAGCCCTGCATGGGTTGTTTGTCTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCT
 ATAAAAATGTTAGAGGAACTTTACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAAAATATTCCGTGG
 TCAAAATCTCTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTTCTGTGAACATGTAAT
 GTAAGTGGCTTTTGGGGTCTCCCAAGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTTCCAGAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGT**GATG**TGGCTTCCGCTGGTGTCTCCTGGCTGTGTCTGCTGCTGGCCGTCC
TCTGCAAGTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGGCCCCAGCGCCCTGGTAAGTGACAAGGAGGCCAGGAAGGTTCTCAAACAAAGC
TTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATGGCAGTGGCTTTGGGG
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGTGGAACAACAT
ACCAAGGCAGGGGGCTGCTGTCAACCTTTGGAAGAATGGCCTTGAATTTGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGGGAGCATTGGCCGCTTTTATCTTGGACCAGATCAGTG
AAGGGCAGCTGGACTGGGCTCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTACAGGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCGTGGTTAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCAGAGCCTGGCTGA
GGTCTGTGAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACGGTGTCAACCCCAACCAAGTGGCTTTTCCATGACAGCCCTGCTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTGCCCTCCACACCATCCCTGT
GATTGACGGGCTGGGGGCGCTGTCTCACAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGCAAGAGCTGTGGTGTGCTAGTGTGAAGAAGGGGATGAGCTGGTGAACATCATATTGC
CCCATCGTGGTCTCCAAGTCAGGACTGTTCACACCTATGAACACCTACTGCCGGGAACGCC
CCGCTGGCTGCCAGGTGTGAAGCAACCACTGGGGACGGTGGGGCCGGCTGACGATGACCT
CTGTTTTCATCTGCTGCGAGGCCACCAAGGAAGACCTGCATCTGCCGTCCACCACTACTAT
GTTTACTATGACACGGACATGGACCCAGGCGATGGAGCGCTACGCTCCATGCCACGGGAAGA
GGCTGGGAACACATCCCTCTTCTCTCTTCTGCTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCGATTCCAGGGCCGTCCACCATGATCATGCTCATACCCACTGCCACGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCGAGTGACTATGAGACCTTCAAAAAC
CTTTGTGGAAGCCTCTATGTGAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCAACCAAGTTCTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGCGGCTGCACCCCTGTGTGATGGCTCCTTGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAAGATCTTCACTGTGGACTGGTGG
GGGCCCCGCAAGGTGCCCTGCTGTGCAGCAGGCCATCTGAAGCGGAACCTGTACTCAGAC
CTTAAGAAATCTTGATTCTAGGATCCGGGCACAGAAAGAAAGAAAT**TAGT**TCCATCAGGGAGG
AGTCAGAGGAATTTGCCAATGGCTGGGCACTCCCTTGACTTACCCTAATGTCTTCTG
CATTAGTTCTTTGACGTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCTAG
TTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGCGCTGTGCATCCCTCACCCATGCCCTCACTCACTGATGATCAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGACGTCAACCTGGTGGGGTTCAGTTC
GTCTCTGAGGCTTCTGCTCTCATTCTATTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACTCAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTGGAGAGCTCTAGATCTCTTTGTGTCTGGGTTGAGTGGCTCTTTCAGGGGACAGGAAT
GCCGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTGATGATCATATCCAATTATCATATGGAAGTCCCGGGTCTGTCTTCTCTATCA
TGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGACCTAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGGTGATGCAGGGGAAGGGTGACATCAGGAGTCAGGGA
TGGACTGGTAAGATGAATACTTTTCTGGGCTGAAGCAGGCTGCAGGGCATTCAGAGCAAGG
CAGAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAGTGCATCAGAAAAAGGGA
AAGCCACGGAATGTGTGGAAGCCAGAAATGGCATTGCACTTAATGACATCATGTGAGGG
TTAGACAGGTAGGTGAATGCAGCTCAAGGTTTGGAAAAATGACTTTTTCAGTTATGTCTTTG
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAAATAAATTTATTG
ATTCCATTGCTTTAAAAA

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FIGURE 64

MWLPLVLLAVLLAVLCKVYLGLFSGSSPNPFSSEDKRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELVNIYCPiVVSNAglFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTkEDLHLpSTNYVYYDtdMDQAMERYVSMpREEAAEH
IPLFFAFPSAKDPTWEDRFpGRSTMIMLIPTAYEWfEEWQaelKGKRGsDYETfKNSfVEA
SMsVVLKLFPQLEgKVESVtAGsPLtNQfYLAAPRGACyGADHDlGRlHPCVMASlRAQsPI
PNLYLTGQDIFTcGLVGALQgALLCSSAILKRnLYSDlKNLDSRIRaQKKKN

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FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCGAGAGGAGGATGCGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGGTGTCTGCTGAGCTTGGCCCTCGGCGTCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGTCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTACGGAAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTCTTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACTGGAATGAAAATCCTTAATGAAGCAA
 TAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCTCTTGAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTTATAGCGGCCACAACCTTTT
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACCTCCTTCAA
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTAAATTCATGGAGTTATTT
 GTGCAGAACTGCTCAGAGAGCTCTACTTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACATTTTTTAATAAA
 ATTATGTCTAAGATTAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPFLFLDKEYDECTSDGREDDRLWCATTYDYKADEKWGFCETEEEAARRQMQEAEEM
YQTGMKILNGSNKKSQKREAYRYLQKAASNHTKALERSVYALLFGDYLQNIQAAREMFEK
LTEEGSPKGQTALGLFYASGLGVNSSQAKALVYYTFGALGGNLIAMHVLVSR

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCCTCTGGCCATGGCCTGCCGGTGCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCACCATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCCTGTGAAAATGGG
TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSQYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

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CGCCGCCCGCCCGGAGACCGGGCCCGGGGGCGCGGGCGCGGGATGCGCGCCCGGGGGCGG
CGATGACCGCGGGAGCGACGCGCGGGGCCCGGCCCTGACCCCGCGCCCGCGCGCTGAGCCC
CCCCCGAGGTCCGGACAGCGCGAGATGACGACCGGAGCCCTTGCTGCTCTGCTGCTCGCCG
CGCTGCTGCTGGGGGCGCTTCCCACCGCGCGCGCGCGCGGAGGCCCCCAAGATAGCGGGAC
AAGGTGCTGCCACGCGAGTGGCGCGCTGGGCGCGCATGTGCGGCTGCAGTGCCTGAGTGGAG
GGGGGACCCGCCCGCGCTGACCATGTGGACCAAGATGSGCCGACCATCCACAGCGGCTGGA
GCGGCTTCCGCGGCTGCTGCCGAGGGGCTGAAGGTGAAGACGTGGAGCGGGAGATGCCGG
GTGTACGTTGTGCAAGGCCACCAACCGCTTCGGGAGCCTGAGCGTCAACTACACCTCGTCTGT
GCTGATGACATATGACCACAGGGAAGGAGCGCTGGGGCCCGACAGCTCTCTGGGGTCAAG
AGGACCCCGCGAGCCAGCATGGGACAGGACCGCGCTTACACAGCCCTCCAAGATGAGGCG
CGGGTGATCGACGCGCGCTGGGTAGCTCCGTGCGGCTTCAAGTGCGTGGCCACGCGGACCG
TCGGCCCGCATACCTGCTGGATGAAGGACAGCACAGCGCTTGACGCGCCAGAGGCGCGCTGAGC
CCAGGAAGAAGAAGTGGACATGAGCTGAGCTGAAGAAGATCGCGCGGGAGGACAGCGGCAATAC
ACCTGCCGCGTGTGGAACCGCGCGGGCGCCATCAACGCCACCTACAAGTGGATGTGATCCCA
CGGGACCCGTTCCAAGCCCGTGTCTACAGGACGCGACCCGCTGAACACGACGCTGGACTTCG
GGGGGACCCGCTCTTCCAGTGCRAAGTGCAGCGACGTCGAGCCGTTGACTCAGTGGCTGT
AAGCGCTGGAGTAGCGGCGCGGAGGGCGGCCAACCTCACCATCGATGGGCGGCCAGAA
GTTTGTGGTGTGCCACCGGGTAGCTGTGGTTCGCGGCCCGACGGCTCTCACTCAATAAGC
TGCTCATACCCGTCGCCCGCGAGGACGATGGGGCATGTACATCTGCTTGGCCGCAACACC
ATGGGCTACAGCTTCGCGACGCGCTTCTCTACCGTGTGCTGCCAGACCAAAACCGCGAGGCC
ACCTGTGGCTCTCTGCTCTCGGCCACTAGCTGCCGTGGCCGCTGGTCTGCTCGCATCGCATCCGAG
CCGCGCTGTCTTCTCTGCTGGGACCGCTGCTGCTGCTGGTGTGGCAGGCCCAAGAAGCCG
TGACCCCGCGGCTTCCGCTCTCCCTGCTGGGACCGCGCGCGGGGACGCGCCGCGACCT
CAGCGGAGACAGGACCTTCTCCCTGTTGGCCGCGCTCAGCGCTGGCCCTGGGTGTGGGCTGT
GTGAGGAGCATGGGTTCGCCGAGCGCCCGCAGCACTTCTGGGCCCGCGCCAGTGTGCTGGT
CCTAAGTTGTACCCAAACTTACACAGACATTCACACACACACACACACTCTCACAC
ACACTACACAGCTGGAGGGGAGGTCACACAGCACTCCACTCATAGTGTAGACGACCGCT
TCTCGAGTGGGACGGGGGGCGCGGCCAGCAGGACGATGGGAGGATGGAGAGCGGAGCT
GCAGAGCGAAGGCGAGGGGACCATGCGGAGGAGGAATGGCCAGCTCCCGAGGAGCTGTGTGT
TGAGGCATAGCCCTGGACACACACACAGACACACACTACCTGGATGATGTATGTAC
ACACATGTGCGCGACACGCTGCTCCCTGAAGGACACAGCTAGCACACGACATGCACAGATATG
CCGCTTGGGACACACAGATAAGCTGCCAAATGACGACACGACGACAGACATGCCAGATA
TACAAGGACATGCTGCTGCTGAACATACACGCGACACCCATGCGCAGATGTGCTGCTGGACA
CACACACACACAGCATATGCTGTCTGGAGCGACACACGTCGAGATATGATTCGGGACACA
CACGTGCACAGATATGCTGCTGGACACAGATAATGCTGCTGTACACACACATGCACGG
ATATTGCTGGACACACACACACACACACGCGTGCACAGATATGCTGTGACACGCGCAC
ACATGCGAGATATGCTGCTGGACACACACTTCAGACACAGTGCACAGGCGAGATATGCT
GCTTGGACACGCGACAGATATGCTGTCTAGTACACACACGACGACAGATGCTGTCCGGACG
ACACAGCATGCACAGATATGCTGTCCGGACACACACGACGACGAGATATGCTGCTGGAC
ACACACACAGATAATGCTGCTTCAACTACACACTACACAGTGCAGATATGCTTGGACACACACA
TGTGCACAGATATGCTGTCTGGACATGCACACGTCGAGATATGCTGTCCGGACATACACG
CACGACACATGCAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACAGGT
CGAGATATGCTGCTGGACACACACAGATAATGCTGCTCAACTACACACAGTGCAGTA
TATTGCTGGACACACATGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATA
TGCTGTCCGGATACACACGCGACACATGCAGATATGCTGCTGGGACACACTTCCGGA
CACACATGCACACAGGTGCAGATATGCTGCTGGACACACGACAGACTGACGTGCTTTTGG
GAGGTTGTGCGCTGAAGCTGCGAGTACGTTGCGCTGAGGCTCATAGTTGATGAGGAGCTTT
CCCTGCTTACCGCTCACTCCGCAACTCTGCGCGCTCTGCTCCCGCTTCACTGCGCCGCTC
CATCCCGCCTCTGTCCCTGGCCTTGGCGGCTATTTTTGCACCTGCTTGGTGGCCGAG
AGTCCCTACTGCTGTGGGCTGGGTTTGGGGGACAGGAGCCCAAGCTGAGAGGCTGGAG
CCCATGGCTAGTGGCTCATCCCGAGTCAATTCTCCCTGACACAGAGAAGGGGCTTGCTTA
TTTATTTTAAAGAAATGAAGATAATATTAATGATGGAAGAAAGACTGGGTTGCGAGGAC
TGTTGCTCTTACCTGGGCGCGGAGCCCGCTGGTCTTTCAGCCATGCTGATGACCACACCC
GTTCAGGCGGACACACACCCCAACCCCACTGCTGGTGGGGCCCGAGATCTCTGTAATTTTA
TGTAGAGTTTGAAGTGAAGCCCGGTATTTAATTTATTTTGTTAACACAAA

FIGURE 70

MTPSPLLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFGGTTSFQCKVRS DVKPV IQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFTVLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTL LLWLCQAQKKPCTPAPAPPLPGRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSTHSHVEGKV
HQHIHYQC

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[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQP GKKNPSIFAKPADTLES PGEWTTWFNI
DYPGGKG DYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQV VHGS PREGFWCLNREQ
RPGQNC SNYTVRFLCPPGSLRRDTERI WSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQH CMGQDCTACDLTC PMGQVNADCDACMCQDFMLHGAVSLPGGAPASGA AIYLLTK
TPKLLTQTDS DGRFRIPGLCPDGKSILKITKVKFAPIVL TMPKTS LKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQ NATNSFY YDVGRCPV
KTCAGQQDNGIRCRDAVQNCCGISKTEERE IQCSGYTLPTKVAKECSCQRCTETRSIVRGRV
SAADNGEPMRF GHVYMGNSRVSM TGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN
KKGS AVFHEIKMLRRKEPIT LEAMETNIIPLGEVVGEDPMAELEIPSR SFYRQNGEPYIGKV
KASVTFLDPRNISTATAAQ TDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKV KVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQR RNKREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYRSE RFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
CVPAFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPR
VKKTA FQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYD YNTVPFN
EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV
NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTAAAAAATATACAGAG
 AATCCATACCCGTACCGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAAGAGATTACAAAGAATTTAGAGATGTATTGTCAAGATCCCTGTCGATTCAATG
 CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTTTGGTTTTGGGGACATTATGATTGTGTAAGACT
 CAGATTTACACGGAAGAAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAAA
 TCTGAAAGTGAAGTCTCGATCCTCCGGATATTACCTGTGGAGACCCCTCCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATTAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTCCTGAGCTGATGTTTGAATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGCTCTGGAGCAAAACCATTTAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGAGCAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATACAGCATACGGCTCTTAGAAATCATTGACACAGA
 AGAGTACTCAACAGGGTATACAAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTCGCGCTTTTGT
 CTGGACCTCGCTACGCAATATGGCTTCCTCTACGGACAGCTGGATACAAACAGAACTCAGAGATTTCTTT
 ACAGTCACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAATATTTGTAGATGAGCTACACTTGGC
 ACGTACTTTTTACGGCATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTCTAATCTCCATGCCACTGTATGTG
 TGTATGACACAGCAAAATGACATGCAATGTGAGCACAACTACAGGTCAGACTGTGGGAATGCAAGAAG
 AATTATCAGGGCCGACTTGGAGTCCAGGCTCCTATCTCCCATCCCAAAGGCACTGCAAACTACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCCGCCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGACGGCACCCAGCGCTGCTGCTGCTGACCCAGCTGCT
 GGGAAACCGCCAGCCCCCTGGTGTCTTAGCTGTCACTCCAGCCACACCGGACGGGCTCTGCGGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAATAGGAAACACACATACAGACACCCCTCCTCAGACAGTGTACAAA
 CTAAGAAGGCTAACTGAATAAGCCATATTTATCACCCGTGGACAGACATCCGAGTCAAGACTGTTAATTTT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAACACATTTGCCAGCTGCAGAGCATATTTGGA
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAAACAACAAATCAACCAGCTAAAAACATTGGC
 TACTCTAGCTGTGGTGCGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTTCTTTGCTGTGAG
 GTGCATTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTTGGCCTGCTTCCCTCCTGAATCCCTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCCCTCGTTGGTTGAAAGATTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAACAGCCCCCTCAAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTTAGAGCACTGAGTCCAGTCCGGA
 GCACACACCCACTATACAAAGAGTGGCTATAGGAAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTT
 ATTTTTCTTGAACTACTGTAATATGTAGATTTTTGTATTATTGCAAAATTTGTGTACCAGACAATCTGTTAAT
 GTATCTAATCGAATCAGCAAAGACTGACATTTTGTCTCTTTGCTGTTGTTGTTTCACTGTGCAGA
 GATTTCTCTGAAGGGCAACGAACGTGCTGGCATCAAAGAATACAGTTTACATATATAACAAGTGTAAATAAGA
 TTCCACAAAGGACATTTAAATGTTTTCTGTGTTTTAACACTGGGAAGATTTAAAGAATAAAACCTCCTGCA
 TAAACGATTTTCAAGAAATTTGATTTGCAATTTCTTAAGATGAAAGGAACAGCCCAAGCAGTTTCACACTCACT
 TTACTGATTTCTGTGTGGACTGAGTACATTCAGCTGACGAATTTAGTTCACGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDL SQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFVTVDLRI RLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCEEHNTTGPDCGCKKNYQGRPWSGPSYLP I PKGTANTCIPS ISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGCTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACCA**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGAGACCTGTGGTGGGAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCTCTCAGATGGAGTGCAGCTTGGAATAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACCTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCAGGAGTTCACCTTGAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTATGATCATATGATTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTAGTCAGGGCAAAACCAT
 TTGTAACAATAAATATTTTGGAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTATATCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGATAAATCTAAAGTGTTTATTAATAAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF
SSFQDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLED TDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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TGCTTCCTGGAGACCCGTGGTGGGAATTACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATATTAGAAAGTGAAGTGGCATT
 TTAACATATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGA AAAAATTAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAAAGAGGGGGGTGGTG
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGGCGGCGTT
 CCTCCCCGCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCAAGTGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACACTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCTATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCCTACCTCTACTCATGCTCTCCTTCCCTTGGGGTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCGCATGTTCTCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCGATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCATTAGGTTGTACTCATCTTTTACCTAATGGTGCTCCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTGCCGCTGCCGT
 CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCACTGACCTCCAGCTGGGGGTGGGA
 AGGAAAAAAGTGGACACTGCCATCTGTGCTAGGCCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGGCCATCTGCATATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCGATCCCAAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGTAGGGGCAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCCTCTGGCCAGCAGAGCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA
 AAAAAA

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FIGURE 79

MEAPDYEVL SVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATV NK
IALELCTFTLAIALGAVLLL PFSIISNEVLLSLPRNYIQLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGV LGRVYETVVMMLLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLP LDMELLHRQVLALQTQ RVLLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVG FY
SSPLFRSLRPRWHD TMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLG NFY
IVFLYNAAFAGLTTLC LVKTFTAAVRAELIRAFGLDR LPLPVSGFPQASRKTQH Q

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAAACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCAATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTCC
TCATGCTGCCCAGGCTAATGTTGAACCTCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGAGACCCCCGCGCCCCCGGTGT
 GAGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGGGCGGAGGAGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCTCTATAAAGGATATTAAGGCGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCCAGCGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGTTCTGTGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACCTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGAATTTGTCGGCAAGAGAT
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCGCCCTGAGT
 TTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTCATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFDLGAAYEVLSDSEKQYDQTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTTPRQQ
DRNIPRGSIIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFGEPEPHVDGEPGLRFRKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTTAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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GGGACGACGAGCGGGCGGGCAGTGCGGCGATGCGCCCGGAGGCCACAGCCTTAGAGCCCTCAGGT
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTCT
TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
TGGACGATGTGTTATACCAACCCCCACATTGAGGCCATTCTGGGAGAATGAAGACTGGATC
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTACACTCTGAC
AGAGAAGCTTGTGGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
TACCCTCCGTTGGACCCCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAG
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
AGTCTCTGTGCGGCTGCTGAGGAGCATTGTGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCTTCGAGGAGCAGTCTGCAATTT**TAGT**GCCT
ACAGGCCAGCAGCTAGCCATGAAGGCCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTACAGCTGTGTGTGCATAG
TAAAGCAGGAGATCCCCGTAGTTTTATGCCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
CTGGTGGACTGTGAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT
AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
TTCTTTTGGCAAGACTTGACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAAT
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTCTCCCGACTCAGCTTCCCACCCTGGGCTTCCGAGGTGCTTTCGCCGTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATGGTTAGAAAGAACATTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAATTTGAAGACTCATTAAAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

FIGURE 90

MISLTD^TQKIGMGLTGFVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
HKMKATGFFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFI^RRPVVLGSL^LLNLP^GI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTCCAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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GGGACGAGGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAGGCTGCCAGGAAGGAGACGCCTTCCTGAGTCTCGGATCTTCTCCTTCTGGAATCTTTGACTGTGGGTAGTTATTTATTTCTGAATAAGACGCTCCACGCATCATGGACCTCGCGGGACTGCTGAAGTCTCAGTTTCTGTGCCACCTGGTCTTCTGCTACGCTTTATTGCCTCAGGGCTAATCATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCATTAAACAAGCAGCTCTTCCGGAGATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGCGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAATGCCATCGTGGTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGACGCTTTGGGCTGTAGGGGGCTCCAAGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAATTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGATCGAAGACGGTTGCCACCAAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTTCTGATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC

GGGCCAAGGGGCTGCCTCGCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATCACCGTGAGGAGCTTGAGAAATGTAGTTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAATAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATGTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCACAAAGCTTACCAGGAGAAGGATGCCTTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCGAGACGCCCATGGTGCCCCCGCGCGCCTGGACCTCTGTAACCTGGCTGTTTTGGGCTCGCTGGTGCTCTACCCCTTCTTCCAGTTCTCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACGCTGGCCAGCTTCATCTCGTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGTGACGGAATTGACAAGGGCTCTGCCACGGCAACTCTGACAGCAAGCAGAAATGAATGACTGACTCAGGGAGGTGTACCATTCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCTCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGCGGAAGTACGACCTTCCAGCCAGGGAGTCTGGTCTCAAGCCGGATGGGAGGAAGATTTTTGTAATCTTTTTCCTCCATGTGCTTTAGTGGGCTTGGTTTTCTTTTTGTGCGAGTGCTGTGAGAATGGCTGTGTGGTGAGTGTGAACCTTGTCTGTGATCATAGAAGGGTATTTTAGGCTGCAGGGGAGGGCAGGGCTGGGACCGAAGGGGACAAGTTCCTCTTCATCCTTTGGTGCTGAGTCTTCTGTAAACCCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTCAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAAAAA

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLELWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFAITVRSRLNVVSAYVDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS
KQKLND

FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTTGCAAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCCTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTTAGTGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGAACATTTTTCTTTGTCAGGCATTA
 CGGACCTTTTTTCCAATTTCTGAATTTCTTCATTGATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACATAACACCACCTCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTT**TGA**TCCTTTTAACTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

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MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEGVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGGEVNEQALKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPQKGLFHRVPLVLANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCCGCGCGGGCGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGCAGCGAAAGCCCGCCGCGCCACACCCTCTGCGGTCCCCGCGGCGCTGCCACCCCTTCCCT
 CTTTCCCCGGTCCCCGGCTCGCGCGCAGTCAGCTTGC GG GTTCGTGCCCGCGAAACCCCGAGGTCAACA
 GCCCGCGCCTCTGCTTCCCTGGGCGCGCGCGCCCTCCACGCCCTTCTTCTCCCTTGCCCGCGGCGCTGGCACC
 GGGGACCGTTGCCGTGACGCGAGGCCAGCTCTACTTTTCGCCCGCGCTCTCTCCGCGCTGCTCGCCTCTTCCAC
 CAACTCCAACCTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGAGCCCTCGGCCCGCTGCCGTAG
 CGCGCTTCCCGTCCGTCCTCAAAAGGTGGGAACCGCTCCGCCCGCGCCGACCATGGCACGGTTCGGCTTGGC
 CGCGCTTCTGTCACCCCTGGCAGTGCTCAGCGCGCGCTGCTGGTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTCGACGCTCTTACGTCTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTTACAAGAAGTTTG
 ATGAATCTTCAAAGAACTACTTGAATGCGAGAAATCCCTGAATGATATGTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTAAAGATCTCTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT
 CGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTTCGCTCAAGGCTTAGCGGTGCGGG
 AGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGTCTCGTGACTGTGAAGCATGTTACAACTACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCCTTCAACATTTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCACGCTGGACGAAT
 TCTCGTCCATCTCTGAAAGTGCCCTTCAGTGTCTCGCTTCAGACCACATCACCCCGAGGAACGCCAACCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAACAGGCCAAGAAATCTGTGCTCT
 CCGTTCGAGCAACGTTTGAACGATGAGAGGATGGCTCGAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACCTGTTTGCAGTGACAGGAAATGGATTAGCCAAACCGGGCAACACCCAGAGGTCCA
 GGTTGACACCAAGCAACGACATATGATCTCTCGTCAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCATACAATGGGAACGACGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAAATGCCACTGACCATGCTGGGAAGAGTGCCATGA
 GAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCACAGGCCTACCTCTCACGTCTCTGCTGCTTTGTTCTCTGG
 TTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCACAGTT
 ATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTTACTATGTGGC
 CACTGGTTTAAAGTGTGCTGACTTTGTTTCTCATTGAGTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGT
 TCCTGCTCCCCAACCAATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTATTATTGTTGTATGTTTTTCTCATTTCGTTTGTGGGTTTTTTTTTCCAACCTGTGATCT
 CGCCTTGTCTTACAAGCAACCCAGGTCCTTCTTGGCAGTAACATGTACGTATTTCTGAAATATTAATA
 GCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMMQDNSVQVSQKVFQGCPPKPLPAGRISRISIESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPNSVCNDERMAAGNGNEDDCWNGKGSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCCATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGCTCTC
TCTAGTGCTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAA

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FIGURE 99

MKVLISSLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTGATGATAATGAAGGAA
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRRLTVVLGLLVLF LTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCCTCTCTGCAGCTGCTGGTGTCTCTTAC
CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGCTGCAGGCTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTGTCTGTCTGTGTCAGAGCCCAAGGAAGTCTCTCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCAAATG
AACGACAGCCCCCTCCCTTGAAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
AAACAATCTTTCCCAAGCTCCAAGGCATCTATTGCTCCTTCCCAGCTCCAATTAGAAC
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAAT
CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCAACGTTTGCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACGGTCAAAAAGTCATGGTGCTGCATCCCTGCCAAGCCCCCTGACCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFM
WQQVFEPWTKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYPLRGT

FIGURE 104

GTGGGATTTATTTAGTGTCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCAAA
 TGCTCTCCGACATGCAGTAGATTGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGCGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAG
 TGATTCCTTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTACGCCCTCTACTAAAGTTGTCTCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGAAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCTGGCT
 GGTAGCATCACAAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCAACAGGCAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAACATAAAGTGAACAGAAATTTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTCCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTTGGTTTTAATTTTGTAACCTGTGGCCTGATCTGTAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNTITNQLKWMKLNVEEGLYSRTLGSITTPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWIIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCCTCTAC
TAAAGTTGTCAATCCGTGGAGCAGGAAA

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FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGACAGGAACGCGGGCGGCCAGACAACGGGC
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTTCGGGGCGCGGGCTGCA
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
TGTCGGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTCAGGAATTGTAG
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTTGAAAAGCATCAGATACAAAATTG
TCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
ATGAAACCTTTAACCTTTGCAAGTTCTACTTGCCAATCTGGGTTCCCAGCGCAAGAAGG
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAATAATGGATGAACTCAATGT
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGTTCCAGT
GCTGGAACCATATTTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
GACCCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
CAGAATTTGAACGTGAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAAATCAAACCTGCTGTTGGTTTTAATTTT
GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAGGTAAGGTAAGGTAAGG
AAAAAA

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FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTCGCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCTATGGGGGCAGCCATCTCCCAGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCACTCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCGTCTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTTACGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAAA

[illegible]

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGWPSPLEPRT

MGAAISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

GTTTGAATTCTCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
GTTCTCTCAAGCAAGTCATTTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
CTCCCTATTTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTTCTAAGTGGA
TCATGTCGGGGAAGAGATACAATCCTTGCGCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
ATGATGTTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
TCAGCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGAATATAAGCCCCT
TTCGGGCATTTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTC
TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTACTTGTTATTTCAACAGAAGT
AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATCCGAGAATCATTGTCA
TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTGCCTTGGAGACTTCATAATTTTTCTA
GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTCCTACTTAGTAGCCC
ATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTGAT
CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
ATGAGGAGGGGAACAGAACTCCAGGCCATTGTGAGAT**ATAGATA**CCCATTTAGGTATCTGTACCT
GGAAAACATTTCTTCTTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
AGTGAATTTTTTTTTTAAAGACCTAATAAACCCCTATTCTTCTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDFPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT
 AGAATAATTTGTATGGGATTTTGTGATGCAGGAAAGCCTAAGGGGAAAAAGAAATATTCAATTCGT
 TGTGGTGAAAAATTTTTGAAAAAAAATTTGCCCTCTTCAAACAAGGGTGTCAATTCGTATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAAGTGTTCCTTGTTTGTCTGG
 TGACTGGAGTACATTCAAACAAGAAACGGCAAAGAAGATTAAGGCCCAAGTTCAGTGTG
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAAGATCATCGATCCTGAGTTCATTGTGAAATG
 TCCAGCAGGATGCCAAGACCCCAATACCATGTTTATGGCACTGACGTGTATGCATCCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGGAGGAAAAATACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT
 ATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGGTAA
 CCTACCATCAGTCTTACATATCTCATTCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACACCTTGCCAAGGCCATCCCTTCTG
 CTGCTTCTACCACCAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGCGGATGTCAAGCTGGGAC
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTCTGTTTTTAAATTGATGGGAGCACCAGCATTTGGCAACCGCGGATTCGG
 AATCCAGAAGAGCTCCGTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGGTCCAC
 TGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACACACAG
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTGGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGCCAATGGAACAGAAGCG
 GGGCTCCCAATGTGGTGGTGGTGTGATGGTGGATGGCTGGCCACCGGACAAAGTGGAGGAGGCT
 TCAAGACTTGCAGAGAGTCAAGGAATCAACATTTTCTTCATCACCATTGAAGGTGTCTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAGGCCGTGTGCAGAACAAACG
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCCCTGCAGCCTCTGGTG
 AAGCGGGTCTGCAGACACTGACCGCTGGCTGCAGCAAGACCTGCTTGAACCTCGGCTGACAT
 TGGCTTCGTATCGACGGCTCCAGCAGTGTGGGGACGGGCAACTCCGCACCGTCCCTCCAGT
 TTGTGACCAACCTCACCAAGAGTTTGAGATTTCCGACACGGACACGGCATCGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCCGACAGTACAGCAGCAAGCCGTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCCAGCAGCAGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGGAGGTCTACGACGACGTCGGATCCAGCCATGGCTGCCCATCTGAAGGG
 AGTGATCACCTATGCGATAGGCGTGTGCCGGGCTGCCAAGAGGAGCTAGAAGTCATTTGCCA
 CTCACCCCGCAGAGACCACCTCCTTTGTTGGACGAGTTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTTCAGAG
 CAGGCAGAGCACCAGCAGTGTCTGCTTTACTAACTGACGTGTGGACACCCACCGCTTAA
 TGGGGCACGACGGTGCATCAAGTCTTGGCAGGGCATGGAGAAACAAATGTCTTGTATTATTA
 TTCTTTGCCATCATGCTTTTTTCATATTTCCAAAACCTTGGAGTTACAAGATGATCACAAACGT
 ATAGAATGAGCCAAAAGGCTACATCATGTGTAGGGGTGCTGGAGATTTTACATTTTGACAATT
 GTTTTCAAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTTATTTCTGATTGAACTCTGTGAACCTCAGCAAGTTTCATTTTT
 GTCATGACAATGTAGGAATTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAA
 AAAG

MRTVVLTMKASVIEMLVLVLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTPSPALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLRPPSPSAASTTISIPRQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGSAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKIQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVCDDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDTDTRIGAVQYTYEQRLFEGFKYSSKPD
LNAIKRVGYWGGTSTGAANFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAAAOEELEVIATHPARHSSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TCCGCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
GCGCCAGGTCCCACGCGCTCCGCGCCAGATCCGCCCCACTACAGTTTTTCTCTGACTCTAAT
TGATGCACTGGACACCTTGCTGATTTTTGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAAACAAACATT
CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGCGGCCCCGAAAACCTCC
TCCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
AACCCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTTCAAGATGTGGCCAGAGTGGCTTTGATGC
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
AAGTGGTGCGCCAGGACGCGAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTGAGATGTACAAGGGGACT
GTGTCCATGCCAGTCTTCCAGTCTTGAGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
AGACATTGACAATGTCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
GGCTCCCGGAATTCTACAAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGCGGAT
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACATGG
GTCCACCTTCGACGCGGTGATACCCCCCTATGGGGAGTGCATCCTGGGGGCT'GGGGGGTACA
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
TCTTCTACCCAGAAAAACATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
AGACTCCTCATAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHGGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPLQSLIGDIDNAMRTFLNYITVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPQT
LFSPENHDQARERKPAKQKVPLLSCPSPFTSKLALLGQVFLDSS

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FIGURE 116

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTCTGAGCTTCTTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCGTGCCACTGTTCTGTCTGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
 TGGTCCTCCAGACACCTTGAAAATAACCAATTCACCCAGAAGTTAATCAGCTGCAGAAGG
 GAGGAGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCTGGAT
 CTCATTAGGTTTGGCGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGACAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAACTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTACAGAAATAAAAAGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLEFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDDVTDITATVPYNLVRVATLGSQTSAW
SILKHFPNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMLILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGTCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAAGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTTCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGCTGCGGCCCTGCGCGCAGCAGGAGCAGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGC GGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
TGGTAGGGGCTTGGGACCCAACCTGTGTCA GTGGAGGAGGTGAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATAACCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTTCTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCCACCAAGGCTTCTGTAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATACTTGTATCAAT
AAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATTATTTTCTTCAATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
AACAAACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAAA

120/330

FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKPTWNEFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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100211-826860

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGGCCTTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCCGGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAGGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGGCCAGGGGCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCCCTTTGCCGGGGACCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAAACAGCAGTTCTGTCTGCCATG
 ACCCCATCAACATCCAGTTACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAG
 GCACATGATGTGTCTGATGTACGGTGCCACCTCATCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCATGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACCCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGT CATGTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCTGCATTGGCTGAAGGACGGGGAGGAGACCCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCT**TGA**ATAAAGCAGCAGGCCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTGCAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTC
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCCTGGATGGGTC
 CGGGAACCTGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCTCCCTCCTG
 TCCATCCCCACATTCCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPTFAHFPEDTVEQKAESVG
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
MNEQGFCCKIVGRSKDMIIRGENIYPAELEDDFFHTHPKVQEVQVVGKDDRMGEEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATGCGCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATGG**ACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTCTGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGACATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCCTGAGCCGGGAGGCCTGCCAGGATACATCGCCGCCGGTTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGTGCCCCCT
 CCAGAGCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCAAGTGA
 ACCACATCCACCACCAAAACCATGCCAGCGCCAACCAAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACTGGACTGGGCTGGCCAGCCCCGTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTGGAGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTTGTGTATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTACTTTCTCCTAGCCAGCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTGCCCTATAGTGAGTCGTA

0995726-112001

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLLRGGAQALECYSCVQKADDGCS PNKMKT VKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCAKLNLT SRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGC FDGNVTLTAA NVTV
SLPVRGCVQDEFCTR DGVGTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTT
VASTTSVTTST SAPVRPTSTTKMPAPTSQTPRQGV EHEASRDEEPRLTGGAAGHQDRS NSG
QYPAKGGPQQPHNKGC VAPTAGLAALLLAVAAGVLL

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100211-0226866

[illegible]

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTQTEVQPSGSLWNLRRLLLEPLDANVDA

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100211-02268660

FIGURE 128

AAACTTGACGCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACCCAATAAAACATTTCCATCCAAA

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100211-0226060

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FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
FLNWHALFESIKRKLPFLNWDAFPKLGKGLRSATPDAQ

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10021-026560

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTTC
TTCTCCAGCCAGTTCCTCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCACATATTAATTGTAACGATTAATAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVVLQPVPTQETGPKAMGDLSCGFAGHS

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100211-022600

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
AAGTATTTATTGACCAAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
TGCAGCTGCTACCATGGTGTCTAGAAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
GACTGTACCGGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
TTGGAAGTGTACGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCA
GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
ATGATATCATGTATCTTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
GCCATGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
ATCCTCTCATTTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCAGAATACACCAAAAAC
CAGGCTTGAAATCTATGAAAGATACTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
GGATCACTGCAAATACAAGTATCTGTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
AACACCTCTTCTGTGTGGCTCACTTGTTCATGTTGGTGATGAGTGGCTAGAATCTTC
TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAACAGATCTCTCCAATGTCCA
AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
TCCCAAAATGTTGAAACTGAACTATAGTAGTCATCATAGGACCATAGTCCTCTTGTGGCA
ACAGATCTCAGATATCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
AAGATTTAAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCAATTTCTTAAGACCAATC
ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTGTCATTTGGAAGTAGTACAA
CTCATTGCTGGAATTGTGAAATATTCAAGCGTGATCTCTGTCACTTTATTTAATGTAGG
AAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATTTCTGAATGGTCTAAGGAAGCGG
TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCAATAAATCTGTTACTCAG
GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

MEWWASSPLRLWLLFLLLPSAQGRQKESGSKWKVFIQINRSLENYEPCCSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEDIAVVFVSFKTSEYHDIMYPAWTFWEGGPVAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAADVHLVDHCKYKYLNFNFRGVAASFRRKHLFLCGSLVFVHVGDEWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCC**ATG**GCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGAGTGGAGTTCGTGCCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGTCCATACCCTAAATTCTGAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCCTCACCCTCCCGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAAGTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFVTS LRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHS LMAAERVKA WTSRYFGVLQRS LYVACTALALQLVMRYWEPI PKGPV
LWEARAE PWATWVPLLCFVLHVISWLLIFSILLVFDYAE LMGLKQVYYHVLGLGEPIALKSP
RALRLF SHLRHPVCVELLTVLWVVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

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100211-020000

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAACTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTCACCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAACCTGCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTTCTTATTAGGCCAAG
 AGGCTGAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAAGTGAAGTTTGGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
 TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAACCCATCAAGTTT
 GAAGATGTTTATGTGGGATCTGTTTGAATTTATTAAGTGAACATTATATTCAGAAGA
 CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACCTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTGATGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGGAGACTGGAGGTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCTCTGTAGACTAGAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTATTG
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGATTACCAATTTAAAAATATA
 TGTAGTTCGTGTCAAAAACCTTCTTCACTGAAGTTTACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATCTTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGACTTTGTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

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FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERNWMYFYEYEPYRQD
FHFTLREHSNC SHQNPFLVILVTSHPSDV KARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVN IHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN
PNKVDDLSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

0000720-112001
10211-026000

FIGURE 140

CATTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTACAGAAGTATA
 TTAAC TTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG
 CTCATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTCCTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTTCCTTTGAGCCTGCATCAGTTCTTGGTTTTCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCTAGCAGTATCTAATTTAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
 CTGTTTTTTCTAAAAAAGT

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FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKRSRSRQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

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FOIb-826860

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATNTTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT
GAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTC**ATGGC**
GGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGCTTCTTCCCTGGAGTACCACTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGACCTCTTACAGAGGCCTACTACTACAT
GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
GGAGGAGACCTTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCTGCGGCTGGC
CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACCAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
TTCTGTGACCAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGAGCGCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
GGCCCTGGGTGGCTGTACTCCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
GGCTCC**TAGC**TGCCTGCAGACCTCCTGGGGCCTGAGGTCTGTCTCTGGGCGAGCGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCGAGGGTGATGTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTAA

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTVDALVLRFFLEYQWVFDAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTSIKMFLTVTRLYFSAEEGERSVCLTF AFLFLLLAMLVQV
VREETLELGLLEPGLASMTQNLEPLLKKQGDWALPVAKLAI RVLAVVGSVLGAFLTFPGLR
LAQTHRDA LTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRWLWLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQORVVRVYCYVT
VVS LQYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAA RI
AGALGGLLTPFLRGVLAYLIWWTAA CQLLASLFGLYFHQHLGAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCGATACAAGCACCCGNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCGCGATTATTAAACGTGGCTT
 AATCTGAAGGTCTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAAGGTGGCCAGGGAGAAATGCAGCACACTGCTCGGAGAAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCTTGGCTCAGTCTGCTTAACACATGACAATGTGGGCAACCTGCACCTCTCTG
 TATTCAGAACTCTGTAAGGTGCCTCCCACTACGGCCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCAAGAGGTTCTGCAGCTGCCACCATCTCCTTTAA
 TGACAGACGAGCCTGGCTTAGACAACCTGCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAAATAATCGAGCTTTGAGTGTTCTTGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAAGG
 GCAGGGAAAAATCTGAAAACCCACTGCCCTGAAGCTTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAA
 ATTACCAGCATCAAGATCAATCGAGTAGATCCCACTGAAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTTCAAAGGTCAAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACAATGGACAGGCCCC
 GGATGCCTACAGACCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGCCCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAAGAG
 TGCGGCTCATCTGATTCAAGCCAGTGAAAGACGTGTTCACCTCGTGTGCTCCCGCCAGGTTCCGCGAGCGGAGCC
 CTGACATCTTTCAAGGAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCCATCCTACAATTACTTGTATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGACGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCACTCAGTGTGTAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCAAGCTGACA
 GAGGTGAGCCGGAGTGAGGCAAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTTGAAGT
 CAAAGAGTATGAGCCCCAGGAAGATGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGCCCCACCCA
 GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCAAGGTGCTTGTATAACTGTAAGATATTTGATTAT
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAAATACAATGGAACAAACCTTT
 TTTTCATCAAAATCCATTGTTGAAGGAACACCAAGCATACAATGATGGAAGAAATAGATGTGGTGATATTCTTCTG
 CTGTCATGTTAGAAATACATCAGGAATGATACATGCTTGTGCTGGCAAGACTGCTGAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTTGGCCTGGCACTTTTTTATAGAAATCAATGATGGGTCAAGGAAAAACAGAAAA
 TCACAAATAGGCTAAGAAAGTTGAAACACTATATTTATCTTGTCAAGTTTTATATTTAAAGAAAGAAATACATTGT
 AAAAAATGTCAAGGAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATATGATTCAAAAAAATTA
 AAACACTAGTGTGTTTTTTCAGTGTGGAGGATTTCTATTACTCTACAACATGTTTTATATTTTTTCTATTCAAT
 AAAAGCCCTTAAACAACATAAATGATTGATTTGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTTT
 GGTATATGCTGAAGTCTGCCAAGGGTACATTTATGGCCATTTTATTTTACAGCTAAAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACACAGAAATAAATATTTTTCAGAAGTTAA

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MKALLLVLPWLSpanyIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
 APSPEVSAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
 FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP
 SESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
 RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDSSFHVILNKSSPEEQLGIKLVRKVDEPGV
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRVQRS
 PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
 WDLPIYVISVEPGGVISRDGRIKTGDILLNVGDVELTEVSRSEAVALLKRTSSSIVLKALEV
 KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNRTAGSLGFCIV
 GGYEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGR
 TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCCAGGCAAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGAATTTCAATCTG
TGCAGACATTCATGTTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAAATTCTTTCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTTATA

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FIGURE 149

MKILVAFLVVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTCTACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTTGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTCGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGAGGACGCAAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCGTATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPTNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALPLRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

100211-026660

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGAATCTTGGCAGTTCACT
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCTTGGA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCTT
TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTTGGTGCTACC
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTTC
TCTTTTGTGGAAAATCAAGTACTTCTTTGAATGATGATCTTTTCTTGCAAATGATATT
GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGATTCTTTCCGTGTCTGAAAGAG
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVTFVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILEPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGAGGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAACCTCAAATGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHELWLLIKREFGFYSKSYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTTGGCAGGTAACCTGTGCACCACCACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCCGCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGTCTCGTGCAATAACCAAGTTAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCAGGCTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAACTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGAACCTGGGCATGTGCAACATTAA
 AGACATGCCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCAATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACCTGGCCCCACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGTCATCTACACCACAACCCCTTGGAACCTGTGATTGTGACATTCCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACAGGCCCTCCTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCCGATGGCAGAACCTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCGCCCACCCAAGGATCTCTGCTCAACGACGGCACCTTGAACCTTTTCCACGTGCTGCTG
 TTTAGACACTGGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCAGGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCACGTCCAATGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTTATATAAACTTCGTAAGCGGCACACGAGCAGCGGAGTACAGTC
 ACAGCCGCCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
 ATGACCATATTAACATAACACCTACAAACAGCACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTCAGACCCA
 TACCAAGGACAAGGTACAGGAACTCAAATAT**TGA**CTCCCCCTCCCCCAAAAAAATTTATAAAAT
 GCAATAGAATGCACACAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLFNLKYLNIGMCNIKDMPNLTPLVGLEELEMGNHFEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLVNSTAELNTSNYSFFTFTVETTEISPEDTTRKYKVPPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLRRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

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FIGURE 158

CGCTCGGGCACCAGCCGCGGCAAGC**ATG**AGCTGGGTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCC
 TTCTCATCTCGTCCTTGCCAAAGAGGTACACAGTCATTAAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG
 TGTCGGGAGCTGTGAATATGATCAGATTGAGTCGCTGCCCGGAAAGAGGGAAGTCGTGGGTATACCAT
 CCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACT
 GCAAGAGCTGCCGAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG
 TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTT
 GTTGGAAAGCTATCCCTAAATGCTCACTGTGAATGGACATTTCATGCTAAACCTGGGTTTGTATCCAACTAA
 GATTGTGATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAC
 CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT
 CCACGTCCTCTTCCATCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT
 GCTCCTCATCCCCCTGTTTCCATGACGCGCAGTGCCTCTTGACAAGGCTGGATCTTACAAGTGTGCCCTGCTTG
 CAGGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAGAAAGAAACTGCTCAGACCCCTGGGGGCCAGTCAA
 TGGGTACAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCGTGGTGTCTT
 TCTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGG
 AAACAGCCCATCTGCATAAAAGCCTGCCGAGAACCAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCGAT
 CGAGGTTCACTCAAGGGAGACACCAATTACACAGCTATFACCTCAGCGGCCCTCAGCAAGCAGAAACTGCAGAGTG
 CCCCACCAAGAAGCCAGCCCTTCCCTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG
 TGGGCGGGCACCATCTGCATCCTTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGACCCAGGGTTGC
 GCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGG
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGG
 GAAGGTCAACATGATCAAGACAGCACTGAAAGTTGTTTGGGGAATTTCTACCGGATGATGACCCGGATG
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTCTGCATCCCAACTATGACCCCATCTGCTTGTATGCT
 GACATCGCCATCTCGAAGCTCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAG
 TCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGA
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCCACTGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTC
 TGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTCTCCCGGACGAGCATCTCTGAGCCACGCT
 GGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCAAGGCTCTCCACTGCCCTTCAACAAG
 GTGCTGCTCTTTAAAGACTGGATTGAAAGAAATATGAAAT**TGA**ACCATGCTCATGCACTCCTTGAGAAGTGTTC
 TGTATATCCGCTGTACTGTGTCACTTGGCTGAAGCAGTGTGGGCTGAAGTGTGATTGGCCTGTGAACCTGG
 CTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATGCTGGTAGGCTGAT
 GCCGCTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAGAGTAAGTTTCTTCAAAGAAGACC
 ATATACAAAACCTCTCCACTCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTG
 ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCC
 CAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTTGTGTACATGGCCACAGTACAGTCTGGTCCTTTCTCTCC
 CCATCTCTTGTACACATTTTAAATAAATAAGGGTTGGCTTCTGAACACAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSVHDGSLHKGAWFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

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FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGAAAAAGCTCAACTGA
 AGCTTTCTTGCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTTCGTGGGTGCCATTCAAGAGATTCTTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCAATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAAACTCTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCGCCGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCAAGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCATTGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCTTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGGTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAAATA
 TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWGWGGE DDLRLRLVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VVRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTGC GCGAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCA**ATG**
 GCCCAGGCAGTGTGGTGC GCGCTCGGCCGCATCCTCTGGCTTGCTGCCTCCTGCCCTGGGC
 CCGGCGAGGGGTGGCCGAGGCTGTATGAACTCAATCTCACCCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATTCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCGGG
 TCTCTGTCTGGGTCACTGCGCGTGA CTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCTCCCCATCACAGAGTTCTCTGTGGGGACCTTGTGTACCCAGAACACTTCCCTACC
 CTGGGCCAGCTCCTATCTCACTAAGACCGTCTCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCCTGAAGCT
 CAAAGTGGTGGCGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAAGTCTCTGGGGAGCCCTCC
 TCTGACTGTGTGTGGCTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCATGTGTACACTTATCACTGTGA
 TGTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAGGTGCTGTGCCAGATGTGTGTGGGCCCTTCTTGTCT
 GGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCTGTCTCCGCCCCCTCT
 ATAAGTCTGTCAAACCTTACACCGTGT**TCAG**CACTCCCCCTCCCCACCCCATCTCAGTGTTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCCACCACTGACCAGGAGGGGTTCATT
 TGCCTGGGGCTGTGGCCTGGATCATCCATCCATCTGTACAGTTTACAGTTCAGCCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTTCGGTGTGACTCCTAGGTGGGCTGGCTGCCACTGCCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTTCTCAGTTTCTCCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCTATAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATAGATGGGCACATCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
 CACACACACACAGAAATATAACACATGCGTCACATGGGCATTTAGATGATCAGCTCTGTA
 TCTGGTTAAGTCGGTTGTCTGGGATGCACCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTGAGTGATGTCAGAGTGCTTTATAAATATCACCTATTTTATCGAAACCATCTGTG
 AAACCTTCTACTGAGGAAAGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG
 TGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCACCTGGCTAACACGGTGAACCCCGCTCTCTACTAAAAAATACAAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCGAACCCGGGAGGCGAGCTTGCAGTGAGCCAGATGGCCCACTGCACTCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

0999720 112001 10211 026650

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFGDGTQ
MVTEDSVVYYNYYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTFRDPGD
YCFsIRAENIISKTHQYHKIQVWPSRIQPAVFAFPFCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMC CGPFLLET PSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCT
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTG
CCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA
TGGCTGTTCTTTTGTTCCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

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1021-026550

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

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FIGURE 166

CTGTCAAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
CTGGATCTTCCACC**ATG**TTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
CCTTGAGAATGGAGCGAGGAGCCAAAGGAGAAGAACCCAGCTTTACAAGCCCTACACCAAC
GGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGCAAGTGG
TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAGT
GAGTCTTGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
GGTCTGTGGGGGTTAGGAGTGCTGATTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGTGGGATACTTGCCAAAT
GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAAATGTGTTACCGGATCTGCGTGGC
AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGATCAGAGAGCCATGGTGAAGGCCTG
CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
CTGAACATGTGCAAGATAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCAT
AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
TGTTGCTATCAAGTATGACCCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCAC
AAGGACAGGAGCCGCTC**CTGA**GCCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGTGCCAA
CGGGCTCAGAGCTGGAGTTGCGCCGCGCCGCCCTGCTGTGTCTTCCAGACTCCAGGG
CTCCCCGGGCTGCTCTGGATCCCAAGGACTCCGGCTTTCGCCGAGCCGACAGCGGGATCCCTGT
GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
CGAGATGCCTTGTCTTTTACATAAGTCGTTGGAGGAATGCCATTAAGTGAACCTCCCCA
CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
CTCTCCAGGAAAGGCACAGCTGAGGCACCTGTGGCTGGCTTCGGCCCAACATCGCCCCAGC
CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGGCTTTCAGCAAAATG
AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTGATCCAGGCTAACCCCTGAACCTCCCC
ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCATCTGTAAATATGAGTCGGGGG
GAATGGTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA
AGGACACATCACGTTTCAAGTACAGGCCCAAAAACGGGGCACGGCAGCCCTGAG
CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTGTGTAGTAAATAAAACTGGCTGGTGAA
TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSFQIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRSQSSKALDNTPEFELSDFYFCRKGME
TIMDDEVTKRFSAAEELSWNLLSRTNYNFYIISRLTVLWGLGVLRICYFLLPLRIALAF TG
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

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10024-22666

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCACCATCCTGCCCTGGGCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTAAGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
AGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKEAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL
YMRHFFPKALHFYLIRALQLLRSGSGCSRGPGEVVFVRGVSRLREFPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTL LLPAGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAGTAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAACTCCTAACATATGCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

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MAGSPTCLTLIYLQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDPDFGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVS RNFS PILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

CTGTGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACCATA
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAAATGAGTCCCATAATGGGTCCATCTCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCACTCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCAGATTCTCCATGGTCTCCT
GTGTCTCCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAA
ACTCTTAACATATGCCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAAATCCCCACTACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTGGAGCAAATCCATGCTCTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCAGAAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCATCCATACAGCATCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAA

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FIGURE 176

MTCCEGWTS CNGFSLLV LLLLGVVLNAIPLIVSLVEEDQFSQNPI SCFEWWFPGI IGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALY CMLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLG LLLVGILEVL FGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GT CGAAT CCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAAGCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATTAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTCCAAAGTCTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FOI# 027660

[illegible][illegible][illegible]

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCAAGGGCAGGCTGTTAGGCCCCTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

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FOI# 024869

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDFFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIP LITPGSATTC

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FOUO-020600

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCC
 TGGCTGGGCGCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCTTCCATTTCAACATCTGAAGTCCCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTGC
 CACCTTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACACCCAAGTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGGCCAGGAACTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCCTGG
 CGTTGATGCTGCTGCACTTCCGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAAA

FIGURE 182

MSLLSLPWLGLRPVAMSEFWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKFWLGEIGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAC
AGTGTGGAGAAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDSEISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAAGTGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

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FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAAT**ATGA**ACACGTGGCTGCTGT
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCACCCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
GTCCCCCGTGTGCGCATGTGTTTACGGGTGAGCCTCTCCAGAAGTGAGATCATGGACAAAA
GGGCAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTAAATGTTCAGA
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTACCCACTAACCA
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
GCATCCCTGCCTGCAGTTGTGGCAAGAACGCCCAGCTCAGAATGAACACACCCACCAAGA
GCCTCCTTGTTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT
GTTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCCTGAGGGTTGA
ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

MNTWLLFLPLFPVQVQLTIVVIGMLVLLDFLGLVHLGQLLI FHIYLSMSP T LSPRSPQGW
V VRAAHLTP LLEYVPNP EPTPGARV FVPRVRMCSG SASPRSEIMDKKGSQE EIKSMRTQQ
AQQEAE LTPRPA GVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTCT
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTAAGTGGGAGACTGGGGATGA
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCCACTCTCCGATTTGGAGGGAA
GCGGTTGATGGAGAAGGCTTCCCTCCCCCTCCCCCTTGGGGCTTTGTGGCAAAAATCCTA
TGTTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCCTGCT
ACTAACAGACTTGCTACTCTACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
CTGTTTCTCTGTCTGTCTGTCTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
TTCGAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAATTATGGCTG
GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCAACCACCTTCA
ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAAA
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGCGGGCTGTCAAGTGCAGCCCCAC
CGTGGGTCTTTGACCAGCTACCACCATGATCATAATCAGCCCATCCACTCTGTCTCTGAGC
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGGCCAGCCAGGAGCTG
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA
GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTCACCCAC
CCCACATCTCACACATCCAGAATTCCTTCTTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
TAAACCATGGAGATAAAAAGAAGAGTAAAAATACACTTCCCGACCTTAAGGATCTGAAA

Figure 1 consists of 11 sub-diagrams labeled (a) through (k), arranged vertically. Each diagram shows a coordinate system with a horizontal axis and a vertical axis. The diagrams illustrate the steps of an algorithm for finding the minimum value of a function. The steps are as follows:

- (a) A point x_0 is marked on the horizontal axis.
- (b) A point x_1 is marked on the horizontal axis, to the right of x_0 .
- (c) A point x_2 is marked on the horizontal axis, to the right of x_1 .
- (d) A point x_3 is marked on the horizontal axis, to the right of x_2 .
- (e) A point x_4 is marked on the horizontal axis, to the right of x_3 .
- (f) A point x_5 is marked on the horizontal axis, to the right of x_4 .
- (g) A point x_6 is marked on the horizontal axis, to the right of x_5 .
- (h) A point x_7 is marked on the horizontal axis, to the right of x_6 .
- (i) A point x_8 is marked on the horizontal axis, to the right of x_7 .
- (j) A point x_9 is marked on the horizontal axis, to the right of x_8 .
- (k) A point x_{10} is marked on the horizontal axis, to the right of x_9 .

The diagrams show a sequence of points $x_0, x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9, x_{10}$ on the horizontal axis, with the minimum value being identified at the end of the sequence.

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFGVTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFSTSLPSCQLGSRRLTTCLE
LWLGLLHGLALLHLHLHGVGCHHLQHVHQDAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTATTTCTGTATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCCTGTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTCAG
GACATTCGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQGGSGME
HRNHLCFCDLYDRATSPPLKCSLL

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GTAGCGCGTCTTTGGGTCTCCGGCTGCGCGTGTGCCGCGCCGCCCTCGGGTCGTGGAGCCAGGAGCGACGTCA
CGCGCTTGGCCAGGCAATCAAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGCATGATGTTTGTAGTCTT
GGATGATGCTGCTTCCAAATATACAACAATATGTCCTCTTTGTCTTATTTTTCATCCTTCACTTATPTCC
ATACTCGTATGACGAAGAAGATTAGTGGATGATACAGATGCTATGAGTAAGCTTGTAGGAATCTGCCATCTTTC
TTTACACGGGCGCATTCGCTGTGCACGTTTGGACTCCCTATGTTATGTTGCTGCAGACAGCATGATTGAGTGGGGA
GCTTTGTGCATCTGTTCTACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGCTCTTTGGAAG
CAATGACGACTTCAGCTGCGCAGCTAGTGGCTGAAGAAGAAATCTATGCAATATTGTCAAATGSACTTCCTGTCAATT
TTGTGCCATTCACGACACAGGAGATGGGCGAGTAATGCTGAATGATGATAGCAAGCTCTGGGGGATTTTTTA
GGTGCTCCCTTCTCACTTTTATGTAGCATATCTTTACAGAGACTTGGCTGAAGGATTAAGAGGATTTTTCT
CTTTTGGAAAGGCTTGACTGATTTACACATTACTATAGATGCTTTTTGTGTGCTCTGCTGAATTTAAATAT
TTATGTGTTTTCGTGTTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTATGTATATCA
TTTGATTGTTGGTAGGAATTCAGAATTCGCGCGCTCTATTACTGGTCAAGTACATCTTTCTCTATAAAATTTT
TAGCCTCCATTTATACAAAAATATAAAATAAGTTTTAGTCAGTCAAGTACATGACATCACTCCCAATGTTATG
CAGACATACAGACGGTGCGTACAGTTATAGACTGATATACAGTGAACATATAGCTCATCTTTATACCTCAGAG
GGCGCAAGTGTTAATGCCATGCCCTCCGTTAAGGGTGTGGTTTTGCTCTGTGACAGATGTTTGTGGATT
AAATTTATTTTTATGGAATTGCTACAGAGGAGTCTTTTTCTTCAATGTTTGAAGAAGATTTATGTTAACTTTA
AGGTAAGGGTGTAAAAACATTTTTGAGATAGGTTTTTTTATTTATTTATTGTTAGAGTGAAGTGCATTTA
GGGAAGAATGACATGAAATTCAGTTTTTGAATCCTGTTTCATTTATAAGTGAATTTGTATCCTCAT
AACCTTTTCATGTTTTACCTGTCTAAATAGACATACATGGAACCACTACTGATGAGGACAGTTGATGTTGTC
ATCATATGCGCAAGAAACCTTCTCTGCTCTCTCTTTGACTATTTGGTATGTGTATATATACATAAAA
TAACCTTTCAAATATAGTTTATAAACACTTGAAGTGTTTACTACCTGAAATAATTTGCTAGCCGCTACAT
CAGAGTGCCGCCCTCCCTCGCAGGCGCTGGCCATGATAACAGTAACCTTTAGTCTTTACAGATATACATGCA
TTAAAGTTTAAAGTTAGACATGTAATAGTAGTTCTTATTCTTAAGGTTATATCATATGTAATTTAAAG
TTTTTTTAAAGACAGTTTCCTGTATACCTCTGAACCTTTTGATTTTGAAGTTCAATCATAGTAGATCTGCTGTT
CTTTTATAAAGGCAATTTGTGTGTAGTGAATGCAAGTAGCCAGTCCAGCTATATAGCAGCTCAGAAAGAT
ACCTGACCAAAAAATCCGAGTACACAGGCATGATCAATTTAGATGTGCTGTTACATCTAAATTAATATCAGGA
CTTTTTTCAGGAGTCGGTTATAAAACATCAAGTGTGCTGACAGATTTTTGTGAAGATATTTGTTGTATG
TTTATTGAGTATACATACATAAAAAATTTTTCGCCATCAGCCAAACCTCAGTAATCATGACAGTCTGTGCTGT
TTTTATGAAGTTTATTCTCAGAAAAATGGAAATAAATTTGGGATTTGTCAGCTTTTTCATAAGATGCTTAA
AGCCACAGGTTTTTTTGCTCAATATAGGCATCTTTAGATATGAGATACGGGAAGCAGGACGAAATATCG
GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGCGCTTGTGTTATATAATGTTAGATTTCAGGAAGAA
GGTGACGATACATGAGTTAGAGAGCTGGTGACAGACTTGGGAAGCTTTGTGCTGTGTGATCTACTGACGTTT
TTTTTGCAGGAAGTGCAATCTCTGCTCTCCCTATTTTCTTGTGATGTGCTGATGCACTGCACTGCTACTG
TTTTTCCACTTGGCCACAGACTTTTTTCAACAGCTCGGTATTTTCTATATACATTTGCAATTTGGCAGCT
GTGCTTTGACCTTGATATAGCTAGCTGACATAGTCTGCTCTGATTTTAGGCTAGTTACTTGAGATATGAAT
TTCCATAGGAATAGCAGCTGATGACAACTACCATCTCTCTATGGAAGAAAACTTTTGATGATGAACAAATA
AGATTTTTAAATATCTATTTTAAAAAAA

TABLE I

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLEVLFYILSPIYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

[illegible]

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDADFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTEHLEHNDLVKVNFAHFPRLISLHSLCLRKNKVAIV
VSSLDWVWNLEKMDLSGNEIEMEYPHVVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPSTG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
LEGALVIINEYGSCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAGGATGGGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCGCCGTTGAGTTCCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTTGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGGCGCGCTTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

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MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPDGLGLVLASGAGFGVSDVGSGLDCGAGEPAVFRSDRSWHDPHLWRSGEA
PGLFFVDAERVPCRHDDVFFPSPASFRVGLGPGASPVVRVSISALGRFTTRDEDLAVFLASR
AGRLRFHGPGLSVGPEDCADPSGCVCGNAEQPWICAALLQP

[illegible]

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGGTTCCGGGGGCGTTCTCCAGTCAACCTCCCGCGGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATAGGGGGGAAAGGACGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTTCCTTCATCTGCTGCATCGAGTGTCTTC
 AACCACCTTTTCTCTCCAACCTAGACCAGCAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCAACGCCCATTTTCATTATATTATGAAATATGGTGTTCCACGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACCTACCCTAACCATTATCTTTGGTAACCTGGCCTCTTTGACAGAGATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTCGGAACAAATCTTCTCCTGGATCACATGAATATTATGATTCCAAGTTTT
 GGAAGAAGCGACACCAATATGGATCACAACACGAGGGCAGGACATAGTGGTGACGCCATGTGGCCCCGA
 ACAGATGAAAAATACATAAGCGCTTCTCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTGAAGATAG
 AGTTGCCAAAATGTTGAATGGTTTACGTCAAAAGAGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCCTGTCATTTGAGATATTGACAAGAGTTA
 GGATATCTCATACAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATCATCACAAGTGATCATGG
 AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCCTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAAATTTGATGAAGTCTATGAAGCACTAATCAGCT
 CATCTTAATCTTACTGTTTACAAAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAAAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTACAGAATAAGTCAGATGACTTCTGTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCCTCAGAAAGAAATTC
 TCAAAAGAAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTGAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCCTGTAAGTGTGTAACACAGCAGAAATATGACCAAGAGGGGTGATACCTTTATTTATAGGGGT
 TCTCTTGGCAGCATTATAGTGATTGTATTTTTTGTAAATTTTCATTAGCATTAAATTCACAGTCAAATACCTGC
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTGCATA
 TTGAAGTGGAGATTCCATAATTTATGTCAGTGTTTAAAGGTTTCAAATTTCTGGGAACCAAGTCCAAACATCTGC
 AGAAACCAATTAAGCAGTTACATATTTAGGTATACACACACACACACACACATACACACACAGGACCAAAA
 ATACTTACACCTGCAAAAGGAATAAAGATGTGAGAGTATGCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCACTTTGCACTATGTAAAGTACCTTATAT
 ATTGCACCTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACCTTTATGGACAGTTATGCTTTATAAC
 TTGATTGAAATGACAACCTTTTGACCCATGTCACAGAATACTTGTACCGATTGTTCAAACCTGAAGGAAATTT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGCAAGAGATGATAAGTGTGA
 AAATTTAAATGTGATAACCTTTGAACCTTGAATTTGGAGATGATTTCCCAACAGCAGAAATGCACTGTGGGCAT
 TTCTTGCTTATTTCTTTCCAGAGAAGCTGGTTTCATTTATTTTCCCTCAAAAGAGAGTCAAATACTGACAG
 ATTCTGTTCAAATATATTGTTTCTGTCTATAAAATATTTGTGATTTCCTGATGAGTCATATTACTGTGATTTTCA
 TAATAATGAAGACACCATGATAATCTTTCTCTATATAGTTCAGCAATGGCCTGAATAGAAGCAACAGGCA
 CCATCTCAGCAATGTTTCTCTGTTGTAATTTATTGCTCCTTTGAAATTAATCACTATTAAATCATTAA
 AAATCAAATGGATAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSVFILAALSLSTTFSLQLDQQKVLVSVDFGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW
ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPFVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAC TGCGGGAGGCCAG
GACAGGCCACCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCCTTGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTCACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
CCTGCCCTTGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGTTTTCAGGTCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTG
TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
GTATCCACTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTTAAATT
ATTTGTCTCCGCCTGAGTCTTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
TGGTCTCATTCATCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
CACACAGCCACCGTGAAAGTCCTGGAGTAAAAATGTGCTGTGTACAGAAGAGAGAAGGAAG
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCCTGACAGTCACTGGCCAGTTA
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTGACAAATAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLKQMNVLAAKIQHLEFS
CSEKPLD

0909720-142001
100211-0246660

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCGGCCAACAT
GCTCTGTCTGTGCTGTACGTGCGCGGTATCGGGGAAGCCAGACGAGTTCACGTACTTTG
AGTCGAAGGGGCTCCCTGCCAGCTGGAAGTCCATTTTCAAGCTACGTGTCTCATCCCTCC
CAGGAATTCTCCACCTACCGCAGTGGAAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT
TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAGCTGA
GGCTGGTGTTTAAGATTTTGGACAAAAAAGATGATGGACGCAATTGACGCGCAGGAGATCATG
CAGTCCCTGCGGGACTTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCACAGAG
CATGGATAAAAAACGGCAGCATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC
ACCCCGTGGAAAAACATCCCGAGATCATCTCTACTGGAAGCATTCCACGATCTTTGATGTG
GGTGAGAATCTAACCGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGATGTGGTG
GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCGGTATCCAGAACCTGCACGGCCCCCTGG
ACAGGCTCAAGGTGCTCATGTCCAGTCCATGCCTCCCGCAGCAACAACTCCGGCATCGTTGGT
GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGCAATGGCATCAA
CGTCTCTAAAATTGCCCGCAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC
TTGTTGGTGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCA
GGGGCCATCGCCAGAGCAGCATCTACCAATGGAGGTCTGAAGACCCGGATGGCGCTGCG
GAAGACGGCCAGTACTCAGGAATCTGGACTGCGCAGGAGGACTCTGGCCAGAGAGGGGG
TGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCTATGCGGGCATC
GACCTTGCAGTCTACGAGCAGCTCAAGAATGCCTGGCTGAGCAGTATGCAGTGAACAGCGC
GGACCCCGGCGTGTGTGCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG
CCAGCTACCCCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGT
CCGGAGGTGACCATGAGCAGCTCTTCAAACATATCCTGCGGACAGGGGGGCTCTCGGGCT
GTACAGGGGGCTGGCCCCCAACTTCATGAAGGTATCCAGCTGTGAGCATCAGTACGTGTG
TCTACGAGAACCTGAAGATCACCTTGGGCGTGCAGTCCGGCTGACGGGGGAGGGGCGCCG
GCAGTGGACTCGCTGATCTCTGGGCGCAGCCTGGGGTGTGCGAGCCATCTATTCTGTAATG
TGCCAACACTAAGCTGTCTCGAGCCAGCTGTGAAAACCTAGACGCACCCGAGGAGGGGT
GGGGAGAGCTGGCAGGCCAGGGCTGTGCTGCTGACCCAGCAGACCTCTGTTGGTTCC
AGCGAAGACCCACAGGCATTCCTTAGGGTCCAGGGTCCAGGCTCCGGGCTCACATGTGTAA
GGACAGGACATTTTCTGCAGTGCCCTGCCAATAGTGAAGTGGAGCCTGGAGCCGGCTTAGT
TCTTCCATTTACCTTGCAGCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGC
ATCTCCCTGTGCCCTCTTGTGCTGCCGTGCTGCTGAGTGAAGTGGGAGGAGGGCTACAG
CCACATCCACCCCCCTCGTCCAATCCCATATCCATGATGAAAGGTGAGGTCAAGTGGCT
CCCAGGCCGTGACTTCCCAACCTACAGCATTGACGCCAAGTGGCTGTGAAGGAAGAGGAAAG
GATCTGGCCTTGTGCTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
TGGGATGCAGGGGGCTCGGGCTGCCCTGGCTGACACAGAAGGCAAGTGTGGGGCTCA
TGGTGCTCTGAGCTGGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAAACCTCACTG
TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATTGTTGAGGCGAAGGGCAGAGCGTTGT
GTGTTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCGCTTAATTATGGAAGTGTGGGAAAAGGG
TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCGTGGGGGTCTCTGCCAAC
CCAGCAGGGGCGCAGCGGGACCGCCACATTCACCTTGTGTCACTGCTTGGAACTTATT
ATTTGTATTATTGAAACAGAGTTATGTCTAATATTTTATAGATTTGTTTAAATTAATA
GCTTGTCAATTTCAAGTTCATTTTATTTCATATTTATGTTTATGTTGATTGTACCTTCCC
AAGCCGCCCACTGGGATGGGAGGAGGAGAGAGGGGGGCTTGGCGGCTGTCAGTACAT
CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGAGCAGCCCTG
GCTCCTTTCTTTGGCAGGTTGGGGAAGGGCTTGCCCCAGCTTAGGATTTACAGGTTTGA
CTGGGGGCGTGGAGAGAGAGGGGAGGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTTC
CTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGAAGTGCCTCC
CATCTGTGAATTTTGTGGTGGCGGGGCTGGAGGAGAGGCTGGGGGCTGGCTCCGCTCCCTCC
CAGCCTTCTGCTGCCCTTGCTTAACAAATGCCGGCCAATGGCGACCTCACGTTGCACTTCC
ATTCACCAGAATCACTGATGAGGAAATCTCAATAGGATCAAGATCAATGCAAAAAT
GTTATATATGAACATATACTGGAGTCGTCAAAAAGCAAATTAAGAAAGAAATTTGACGCTTAG
AAGTTGTCAATTTAAGCAGCCTTCTAATAAAGTTGTTCAAAGCTGAAAAAAGAAAAA
AA

0998728.14204

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFI PSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQA SIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTCAAGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCAGCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTGATGTGAAGTACAGCAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGATCCCCAGATCTCAGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPPQPTVWVASQVD
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTSEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

6
5
4
3
2
1
0
1
2
3
4
5
6

[illegible]

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPILLKRASAGLQRVHEPTWAQQLLQEMKTLFLNTEYLMPFLLNQCSSLYYTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFFILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGCAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAAGTGCAGTGAGGAGACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCGTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTT
 CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTGGAGGAGTCA
 TCTTTGAAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTTGAGGTCCCTGGGGCTGCACTTTGCCCAGCACCCCATTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTTCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGCTCCTCAGGCAATGCCGACAGCTGCCTTGTCTTCATTATTA
 AAGCACTGGTTCACTTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

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 10021-826560

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

0909720-112001

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCTCACTGGCCACCTCCCAACCCCAAGAGCCAGCCCCATGGTCCTCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGTGCTGAATCTGGGTCCCCGGCGGGCGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCAGTACCAGGACCACCCTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAAACGGGTCA
 GGATTGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTAGTATCTCAACCTCT
 CTGCCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAACAAAACCTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLLNLGPRAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMFPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTFPFTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

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FIGURE 215

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGG**ATGG**CCGGCCTGGCGGCGCGGTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGGCGAGCGGCTCCCAGGGGACCGGTAGCCGCGGTATACCGCGACTGCGTACTGCAGTGCGAAGAGCA
 GAATGCTCTGGGGGCGCTCGAATCACTCCGCTCCCGCCAGCCAACTACAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTCCACCGTTGGGCTCTACCTCCAGGAGGTACAAAGTGCCT
 CAGTTCATGGCAAGTGGCCCTTCTCCCGGTTCCGTGTTCTTCAAGAGCCGGCATCGGCCCTGGCCTCGTTTCT
 CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACA
 CCTGTGTGGCCTTCGCTGGGTGTCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTCTACCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGACGCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGTTGGCCAACGTGGCTATTGGCCTGCTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCTGTGGAAACAGCGGCGGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGACGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCCGCTCTTCTGGGCTCCTGGATGCCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGTCTCTTTTTCAGCTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGAC**TGA**AGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCCTCCCAGCATCTGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACCTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCGTGTTTCTCCCAACAGCCTCTCCCACTCCCCAGCTG
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACCAAGGCCTTAGGGATACAGGGGTCTCC
 CTTCTGTTACCAACCCCAACCCTCCTCCAGGACACCACCTAGGTGGTGGTGGATGCTTGTCTTTGGCCAGCCAA
 GGTTCACGGCATTTCTCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTTGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGCTCCAGCAAGCCAGGGCA
 AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCCGTGAGCATGGCCCTGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGT
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGCAAGGGGTGGGTGTGTAGCGTGGGTTAGGGGAACGTGTG
 TGCGCGTGTGTTGGGATGTGAGATGAGTGACTGCCGCTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCTGTCAACATCAATAATCACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCTGTCTGGTGGCCCTTTGCCCGCTCTCTGCAAC
 CTCACAGGTTCCCAACACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAGGAGAAGAAAATGGGGATGGC
 TGGGGCTCTCTCCATCTCTTTTCTCCTTGCCTTCGATGGCTGGCCTTCCCCTCCAAAACCTCCATTCCTCT
 GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGAGGAGGAAGGGCGATTTGAGGGAGAAGGGGAGAAAAGCT
 TATGGCTGGGTCTGGTTTCTTCCCTTCCAGAGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCC
 ACACATATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTACACAGCAGCCCTGGCATGTTCTGCCCCACAGG
 AATAGAATTGGAGGAGCTCCAGAAACTTTCATCCCAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGT
 CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG
 GCCTGCGCTAGCTTCTTTGATACTGAAACCTTTTAAGGTGGGAGGGTGGCAGGGATGTGCTTAATAAATCAA
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

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FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDSDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHFAVVSFAFRALLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWVWLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCCGCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA
CT**ATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC
TGGATGCCGAAGTCTTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAA
ACTCCAATATGAGGACAAGTTCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGGAAGAGAAGATTGCTGCGCTC
TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG
TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCTCGTGAAGGAGTATGCTGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGTCCAGGTGGAGGCCATCGAAGGGGGA
GCCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
CCTGTTTGCACGTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCCAGCGGCAGTTCTGAAGC
TCGGGGGGCTGCAGGTCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGGTACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGA
GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT
GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCCTGCCGGGACCGCTACCG
TCAGGACCCCGAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGAT**GAG**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
GGCTGAGGGGTGCCAGCGTGGTGGGCTTCTCAGGCAGGAGACATCTTGGCAGTGCTGGCT
TGGCCATTAAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEEEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGRDLINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQM DNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPVKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRTLVQEKGTEVLAVRVVTLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTTCAGGCCCCCACCCTCC
 TTCCCACCTGACCAGC**CATG**GGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGC
 CCGGCCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGT
 CGCAGGGGCATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTTCATCTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCTTCCGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCATTACTTCTCGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCCTGGTGGTTGGGAGTCACCTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTTCAGCGCAGCC
 TCTTGTAAGGACT**TGA**CTACCTGGACTGATCGCTGACAGATCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTTCAGCCAGTCACTGACTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT
 GGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCGGACAGTGCAG
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGAGGGAGGAGGTATATTGGAACCTTTCTAACCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTAACTT
 CCTTAACCACCAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGG
 GAGATTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGCGGGGAGGTTTTCTATAAACTGT
 ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAATTTGTAAAAA
 AA

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FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSFYYFLTSAFLTAIIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGCTTGAGTGAGGACGGAAGATCAACCCA
TTTCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

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FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCC GGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

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GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCNNTCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAGGCCCCCAACCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTTCGTCGCGTTCGGGCCCGGCCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTGGTCGAGGGG
ATTTTCTGCGTGGTCTCCCTGCTCCTGGCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTG
CTTCTACAGGAGGTGTTCCGCTTGGCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTACGGCCGCCCCTGCGAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCTGGCTACTCCACCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACGAACAGAAGAATTGCTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCCCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCCTGGGGAGATTACCCTTGTCGCCGGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGAG**TCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGG
 GAACAATTTCCAAAACCTGTCCAGGGCGGGGGTTCGGTCTCAATCTCCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA
 CTGAGAAGTGGAATAAAAAA

FIGURE 226

MATARPPMWWLICALITALLGVTEHVLANNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGDSGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

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FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATTGGGCGGCGCTGCCAACTTGAGGACCGGCGCGCGA
 CAAGCCGACGAGCGCGAGCTGGGCTACGTGCTGTGCAACCGTGTGCTGGCCCTGGCTGTGC
 TGCTGCTGTAGCTGTCAACGGTGCCGTGCTTCTTGAACACGCGCCACGCGCGGCGACG
 GCGCCCCACCTGTGCTCAGCACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCGACCTCACCGACA
 GCTTCGCACGCGCTGGAGAGCGCCAGGCGCTCGTGCTGCAGGCGCTGACAGAGCACCGGCC
 CAGCCACGGCTGGTGGGCGACAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC
 CCGGCTGTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGATGGGGCTGCCGAAGGGGATG
 GCACGCTGGGGCAGGGCCTCAGCGCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTACGCACATCCTGGATGCCCT
 GCAGAGGGACCGGGGCTGGGCGCGGCCCGCAACAGGCCGACCTTCAGAGAGCGCCTGCC
 GGGGAACCCGGCCCCGGGCTGTGCCACTGGCTGCCGGCCGAGACTGTCTGGACGCTCCTC
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTTCCCAACCACTACCGCGCGGCTT
 CCAGGTGTACTGTGACATGCGCACGGACGGCGCGGCTGGACGGTGTTTCAGCGCGGGAGG
 ACGGCTCCGCTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCAACAGGCTGCCCTACGAGCT
 GCACGTGGACCTGGAGACTTTTGAATGGCACGGCCCTATGCCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTTCCTCGTGGACCTTGAGGAAGACGGGTACCCGCTACCGGTGGCTGACTATTCC
 GGCACGTGGAGCTCCCTCCCTGAGACAGCGGCTGAGGTTCAACCAACAGGACCTTGA
 CAGCGACCACTTCAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCTGTGGTACCGCACT
 GCCACAGCTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCTCCATGCGGACGGC
 TGGAGTGGTCCCTCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCCGCTCCGGGAGGACCGCTAGACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTGCG
 CCCATCCCCGACCCCACTCACTCTTTCTGTAATGTTCTCCACCCACCTGTGCCTGGCGGAC
 CCACTCTCCAGTAGGGAGGGGCGGGCCATCCCTGACACGAAGCTCCCTGGGCGGGTGAAGT
 CACACATCGCCTTCTCGCGCTCCCCACCCCTCCATTTGGCAGCTCACTGATCTTGTGCCCT
 TGCTGATGGGGGCTGGCAAACTTGACGACCCCCAAGCTTCTGCTGCCCTGCCCCACTGTGACTCCG
 TGCTGTTTCCGCTCCCTGGCAGGATGGTGGAGTCTGCCCGGCTCCCTACCTGCGCTGCC
 GGCCAAATACCGGCATTATGGGGACAGAGAGCAGGGGCGAGACAGCACCCCTGGAGTCCCTC
 CTAGCAGATCGTGGGGAATGTCAGGTCTCTCTGAGGTCAAGCTGAGGGCAGTATCCTCCAG
 CCTCCCAATGCCAACCCCACTCCCGTTCCCTGGTGCCCGAGAACCCACCTCTCCCCAA
 GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTAGGATGGG
 GAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAAGTTCCCTGGAGGCCACCCAC
 CCGTGTGCCCGGCGAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG
 TCTCAAATGAGGCCCAACCACTCCCCACCCAGCTCCCGGCGCTCCCTACCTGCGGCGAGC
 CGGGCTGCCATCCATTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTTTGGTTTCTGGGCTGGGGCTAGGACGGGCTGGGATGAG
 GCTTGTGACAAACCCCAACCAATTTCCAGGGGACTCCAGGCTCTGAGGCCCTCCAGGAGG
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCTTTGCC
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCGCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCACCGGGCAATGGGGTTCGGGGGAGTGGGGCACAGACCCAGGCACCACTGGACA
 CTTTCTTGTGTAATCCTCCCAACCCAGCACGCTGTATCCCACTCCTTGTGTGCACACA
 TGCAGAGGTGAGACCCGAGGCTCCAGGACAGCAGGCACAAAGGCGAGGGCTGGAGCGGG
 TCCTCAGCTGTCTGCTCAGCAGGCTGGACCCGCTGCGGTTACGTGAGGCCAGATGCAAGG
 CGGCTTTTCAAGGCCCTCTGATGGGGGCTCCGAAGGGCTGGAGTACGCTTGGGAGCT
 GCCTAGCAGCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTTCCCAAGAGCACCCGATGGCA
 GGTGCCCTAGGGGGTGTGGGTTCCGTTCTCCCTTCCCTCCCCTCCACTGAAGTTTGTGCTTAAA
 ACAATAAATTTGACTTGGCACCCTGCGGGGTGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCAGTGCCACCAAGGTATCCACATGCGCAG

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MVNDRWKTMGGAQLEDRPRDKPQRPSCGYVLC TVLLALAVLLAVAVTGAVLFLNHAHAPGT
 APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
 QPRLVGDQEQLLDTLADQLPRLRARASELQTECMGLRKHGHTLGQGSALQSEQGRLIQLL
 SESQGHMAHLVNSVSDILDALQRDRGLGRPNKADLQAPARGTRPRGCATGSRPRDCLDVL
 LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFRRGWDAYRDGFGRLT
 GEHWLGLKRIHALTTQAAAYELHVDLED FENGTA YARYGSFGVGLFSVDPEEDGYPLTVADYS
 GTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSLNKGQYLRGAHASYADG
 VEWSSWTGWQYSLKFSEM KIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCCGCGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAAGT
 TTCCATATTATAATAGATGTACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCTCTGCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTTCTACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTCTGTTCATTAAAGACTCTGATAATTG
 TCTCCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATCCCTTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCATTTTCTTCCATTGACCCATATTTATACCTTTTCAG
 GTACTGAAGATTTAATAATAATAATGTAAATACTGTGAAAAA

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FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNNTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCACTTCCC

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CCGCGAGCGCAAGAACCTGCGCAGCCAGACGAGCTGCTGGAGGGGAATCGAGGCGCGGCTCGGGAGTTCGGCTCGGGCGCGTGGCTGCTCTGCTCTCGGGGAGGGAGCGGGCGCGCCCGGGGCCCAGGACCCCTCGGATCCGCGCCCTCCCGGTCCCGCCCTCGGAGATCCTCTGGTGCTGCTGGGGGTTTCGGCGGGGCGGGGACCCGCGGTCCGGGCGCCATGCGGGCATCGCTGCTGCTGTGCTGTGCTGGCGCGCAGGCGCCGTGGCGCTGGGCATTCCTTGGGCTTCACCTGAGGCCTGCTACAGCTCACTTGGGTGGAGGACGCTGCGCGCCGCCAACCTGGAGACTCTGAGCTGCCGCGCGCGGCAACACCAACGCGGCGCGCCGGCCCAACTCGGTGCAGCCGGAGCGGAGCGGAGAGAGAGCCGGGGCGCGGGAAGGCGCGGGGAGAATTTGGGAGCCGCGCTTCTGCCCTACACACCTTGACACGCGCGGCGAGGCGCCGCAAAAGGCCGTGAGGACCCGCTACATCAGCCGGAGCTGGGCATCAGGCAAGGCTGCTGTGTGGCGGCTGATCATCTCAGACACAGCTGCCGCCACGCTGGGCGTGAACCCGACCGTGGGACCCGCTGGAGCGCTGTGGTGTCTTGACGGGCGCGAGGGGCGCGCGGGCCCACTGGGACATGGCAGTGGTGAACGCTTGGGGTGTGCTGTGCGGATGCTGTGCAACCACTTGCGCCCACTGGAAGGCTGCGCAACGACATGCTAGTGCGCGCCCTGACGAGTGGCTGGGTGCTGCTATCTCGATGCCACGGGGTGGGCTGCATGGTGAGGACAGGGGGGTGCACTATGACCATCTGGAGCTGAGCCCTGGGAGCCAGTGCAAGGAGGACCCCTATTTCCGAAGTGCCCTGACAGCCACCTGTGCGTGAGCCGTGGCATGTACCAGCTGCACAAAGCTTTTCGCCCGAGCTGAATCGGAACGACGATACGAGGATCAGAGGTACAGTGGGAGATCCAGAATACGACCATCTGGCCGCTTGATGGGAGCCGGGCGAGCTTGCTGGCCGCTGGGTATTCCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACATCTTCAACGAGCAACGACGCTTTCTTCTGCGCCAGTGGCTCACCCGCTGCCCAGCTGGCTGGGGCTGACCGGGCTCATGTGGCCGATGTTCTGGGAGACGCTCTAGAGGAGCTGAACCGCGCTACCACCGGCCCTTGCGGCTCCAGAAAGCAGCATGGTGATGGGTACCCAGCGCTTGTATCCGCGCCGGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCAAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCCAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCCAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCCAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCCAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCCAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCTCTACTGTGCTGCTGCTCTAGCTGCGGTGAGCGTGACCTGGCCCTGGCTTCTTGAGGCGCTTGCCATCTGACAGCATGGAGCTGGGTGATGCTGCGCGAGCCCTGACCTGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATCAGATGCTCTTCGCACTGTCAAGGCCCACTGTGCGACGCTGGAGAGGCGGCTTTCCCGGTGCCCGTGTCCATGGCTCAGTGTCAGACAGCGCGCACCTCACTCACTGCGCTCTATGATCTCAAGAAGCACCCGCTGGACACACTGTCTCTGCTGGCGGGCGAGACAGCGTGCTCAGCGCTGACTTCTGCAACCGCTGCCGCTGATGATGCTCTCCGCTGGCAGGCTTCTTCCCATGCTTCCCATGCTTCCAGGCTTCCACCGAGTGTGGCCCAACCAAGGGCGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCTTTGATCGCGCAGGCGAGCCAGGCGCTGCTTCACTAACCTCCGATACGTTCCGCGCGGTGGCGCTGAGGCTGCTGCTGCGCGCGTGGAGCGGCGCTGCTGCAGCGCTACCGGGCCAGGCTGACGCGAGGCGCTCAGTGAGGACCTGTATCCACCGCTGCTCCAGAGCTGTGTTTGAACAGGAGCAGGGCAACAGCACTTGAACCCACCTGTGCCGCTGGGCGTGGCATGGCATCAGGCTGATCCGCGCCCGGATATGGAATATACACGTGAGCTTGAGCTGGAGGCATGACCCCCAGGAGGCCGCGGCCCTCACTCCGAGTGCAGCTGCTCGCGCGCTGAGCCGCGTGAGGAGCTGGGATCTTGCTGTGCCCTATGTCACTGAGGCTCATCGCT

FIGURE 233

MRASLLLSVLRPAGVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPHYPAQPGQAAKAVRTRYISTELGIRQLLVAVL
TSQTTPLTLGVAVNRTLGHRLERVVFLTGARRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGGDFDWFVLVPDTTYTEAHGLARLTGHLSLASAAHYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCNRDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGI PAPS RPAS RFVL RWDY FTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPVYTEASRLTVLLPLAAAEERDLAPGFLEAFATAALEPGDAAAALTL LLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPRLMDLLSKKHPLD TFLLAGPD TVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHGPVAPPQGGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSHLVLR AVEPALLQRYRAQTC SARLSEDL
YHRCLQSVLEGLGSR TQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGAGAGAAAGGAGT
 AGCTATTAGCCAATTCCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCCTCATTGGAACCAAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCGCCCCCTGAGACCCTGCAGCACCATCTGTCA**ATGG**CGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGCGCCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAAGTCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TC**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

MAAGLFGLSARRLAAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKPVL DVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCCTTTTGGCGGCAGCGGCACGCGAGGGC
TCCCGGCCGCCCGCGCTCCGTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGCCCCAGAACCAGACCACCCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCTGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGACGCGCTGGGATTTCGGAGCTTACGCGGGAAGGAGTG
 TCCCATACAGGCTCTTTCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATTCACACAAGGCTTTTGAGGACCCGATACTGGGGGCCACCTTCTCTGC
 AGGCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAGTACCACTCCCAAGGCAGTGATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCACTTGTATTTGATGCCTTC
 ATCACGGGGCAGGGAAGAAAGAACTGGTCCCTCTTCCGGATGTCTCCCGAACCTCACGGA
 GCCCTGCCCTTGGCTTCAGAGAGCCGAGTCTATGTGGACATCAACCTACAACCAAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCACTTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCAGTGCCCTTCTGTC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACTGCTGTAC
 AACACCAACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGTGCAACCCACCTCCTGGAGATGCTGATTCACTGTCGCG
 GCCAAGTCACTACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTAGCCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**TGATT**
 CTTGCCCTTTCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGTCTCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAAGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTTGAATTA
 CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACCTGTGTAGTGGA
 TGGAGTTTACTGTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAAAAAAA

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MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATQFQFTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVCTENITPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTLSSVVFDAFITG
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPVPVFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLDTPVPWYLRLYVHTLITSKGKENKPSYIHYQPAQDRLOPHLEMLIQLPANS
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLPVSD
GSNYFVRLYTEPLLNLPTPDFSMYPNVICLTCTTVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

CAACATCGGGGTCCAGCAGCTTCTTGGTCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCACGCTGACAACTACGC
TGCTTCAAGTCCGATCCTCCCAGTGTCACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATGATGCTGGGTCTTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCTTGAGACTTGGAATATGGAAGAAGCAATACCCAAAC
CCACCAAAGAAAACCTGAGCTTGAAGTCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGAGCTAGAAGGCAGTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGAAGTCTCCAGCCTCTAGAAGTGTGAAGAAATAAATAT
TTGCTGTTTTATAATCCAA

FIGURE 240

MGSSSFVLVMVSLVLTVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEgGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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1002118248660

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATGTGTTAAGACAAAGGGTGTGCACCTTCTTGCCACGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**CTG**AGGTCCTGCCTGTGGAGATGCAGGACCTGAGCCAAAGG
 CGTCCAGTGGTCTCTTGCTTCTGGCTGTCTTCTTCTTCGCTTCGCCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGGCCAGAAAAAGAGAAAACCATGTTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCCAATCATGGAAGAGCC
 AGGACACAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACACAGCCAAGACGCTCATTCCCAAAAGTCA
 GCACAGAATGTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTCCAG
 AGCCCCACGACGCAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTCTGCCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCAAC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTCCTGGAAGGCAC
 CCGGGACTATGAGTGGTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGCTACACGATGAAGGATAATCCGGCTGTACCAGCGCTCCTGGTC
 CCGGAACCTGCCAAAGCCAAGAACT**CTGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCGAAGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAAATGGCTAATTGAGGTTCTGAAGTCTCTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTTAATTAATGGGGTGATGGGTGGCCAATACCACAATTCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACCTCACTAC
 AGATTGCTAGAAAGACCTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACCTGTCTCTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAGGCCAAATAAATTTTCTACAGTGAAAAA

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FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSPFIKEPQTKPSRHRQRTENIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQDTKTTQGNNGGQTRKLTASRTVSEKHQG
KAATTAKTLIPKQHRMLAPTGAIVSTRTRQKGVTTAVIPPEKKPQATPPPAPFQSPTTQRN
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
NQSEWDRLEHFAPPFGFMELNYSLVQKVTRFPPVPQQQLLLASLPAGSLRCITCAVVGNGG
ILNNSHMQEIDSHDYVFRSLGALIKGYEQDVGTRTSFYGFTAFLTSLLILGNRGFKNVP
LGKDVRYLHFLEGRDYEWEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
RYMKNRFLRSKTLGDAHWRIRYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYIDTSW
KRLIFYINHDFKLEREVWKRHLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

000000-100000

CG ATGCGCGGACCCGGGCACCCCTCTCTCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAGTGCAGCAAACTTCCATAGACTTTATCACAA
CCAGAGACTGCACCATTCTGCATACTATAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAG TGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGAAACCAACAGGGAAACAGAAGTATCTTTATACATCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATT

[illegible]

FIGURE 244

MRGPGHPIILLGLLLVLGPSPEORVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT

RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGGCCCGCCGACAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
CCCGACCCCGGCCGCGCCAGCCCCACCA**ATG**CCACCCGCGGGGCTCCGCGGGCCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTTGGTGCTGGCCGCGGAGGACTGCCT
GTGGTACCTGGACCGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTGTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGACGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
ACTATAGGGGTTGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCGTGTTTCAAATAGTCCCTCTGCTCCCAAGATCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MP P A G L R R A A P L T A I A L L V L G A P L V L A G E D C L W Y L D R N G S W H P G F N C E F F T F C C G T C Y H R Y C
C R D L T L L I T E R Q Q K H C L A F S P K T I A G I A S A V I L F V A V V A T T I C F L C S C C Y L R R R Q Q L Q S P
F E G Q E I P M T G I P V Q P V Y P Y P Q D P K A G P A P P Q P G F M Y P P S G P A P Q Y P L Y P A G P P V Y N P A A P P P
Y M P P Q P S Y P G A

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGCAAGGGTGAGGGCGGGCCAGAA
 CCCCAGGTAGGTAGAGCAAGAAGATGGTGTCTTCTGCCCTCAAATGGTCCCTTGGCAACCATG
 TCATTCTACCTTTCTCACTGTGGCTCTCTTAAGTGTGTCCACTCCTTCATGTGTGCAGAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCAATTTCTTGGAAATAAAATACGACTTC
 CTGAGTACGTATCCCAAGTTCATTATGATCTCTTGATCCATGCAAAACCTTACCACGCTGACC
 TTCTGGGGAACCCAGAAAGTAGAAATCACAGCCAGTCAGCCACCAGCACCATCATCTGTGCA
 TAGTCAACCACTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCTCGAGGTCTTGGAACACCCCCCTCAGGAGCAAAATGCACTGTGCTGGCTCCCGAG
 CCCCTCCTTGTGGGCTCCCGTACACAGTTGTCTTCACTATGCTGGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAACAGGATACCTAGCAT
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAAATAGAAGAGAGCAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAAATCTGTGACTGTGTCTGAAGGACTCATAGAAGACCATTTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTTCAGATTTTGAGTCTGTGCAGCAAGATAAC
 AAGAGTGGAGTCAAGGTCTTCTGTTTATGCTGTGCCAGACAAGATAAAATCAAGCAGATTATGC
 ACTGGATGCTCGGTTGACTCTCTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCC
 TACCCAAACAAGATCTTGTCTGCTATTCGCCACTTTCAGTCTGGTGCTATGGAAACCTGGGA
 CTGCAACATATAGAGATCTGCTCTGTGTTTGTATGAGAAAGTCTTCTGCATCAAGTAA
 GCTTGGCATCAGAGTACTGTGGCCATGAACCTGACCAAGTGGTGGTGGGAAGCTGGTCA
 CTATGGAATGGTGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGAGTGTGTG
 TCTGTGAGTGTGACCCATCTGAACTGAAAGTTGGAGATTATTTCTTTGGCAATGTTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCCTGTGTCTACACCTGTGGAAATCTCTG
 CTCAGATCCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGGAGCTTGTATTTGAAATG
 CTAAGGGAGATCTTTAGCGCTGACGCATTTAAAAGTGGTATTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG
 ATGGTGTAAAAGGGATGGATGGCTTTTGTCTCTAGAAGTCAACATTCATCTTCATCCTCACAT
 TGGCATCAGGAAGGGGTGGATGTGAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT
 TCCCTTAATAACCATCAGAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCATACATGA
 AGGGCTCTGACGGCGGCCCGGACACTGGGTACCTGTGGCATGTTCATTGACATTCATCACC
 AGCAAAATCCAACATGGTCCATCGATTTTGTCTAAAAACAAAACAGATGTGCTCATCTCCC
 AGAAGAGGTGGAAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTACATGTGCATTCAG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTCATTAAACAATGCATTTCACTGTGTCAGCTTGGGAAGCTGTCCAT
 TGAAAAGGCCTTGGATTATCCCTGTACTTGAAACATGAAACTGAAATTTATGCCCGTGTTTT
 AAGGTTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTCAAGGCTTCCCTCATCAGGCTGCTAAGGGACCTACTTGATAAGCAGACATG
 GACAGACAGGGCTCAGTCTCAGGCAAAATGCTGCGGAGTGAACCTACTCTCCTGCCTGTG
 TGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTTCAGAAAGTGGAAAGGAATCC
 AATGGAAACTTGAGCCGTGCCGTGCGACGTGACCTTGGCAGTGTGTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTCTTATAGTAAATATCAGTTTTCTTGTCCAGTACTGAGAAAA
 GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAAATAAAAACCTCAGGAGTTTCCACAAAATCTTACACTCATTTG
 CAGGAACCCAGTAGGATACCCCACTGGCCTGGCAATTTCTGAGGAAAACTGGAACAAAACCTTG
 TACAAAAGTTTGAACCTTGGCTCATCTTCCATAGCCCCACATGGTAAATGGGTACAACAAAATCA
 TTCTCCACAAGAACACGGCTTGAAGAGGTAAGAGGATTTCTTCAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAAATTTGAACCAATTTGAAGAAAACATCGTTGGATGG
 ATAAGAAATTTTGATAAAATCAGAGTGTGGCTGCAAAAGTGAAGAGCTTGAACGTATGTAA
 TTCCTCCCTTGCCCGGTTCTGTATCTCATATCACCACATTTTGTGTAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTCTCCCTCAACTCATTTTTTGA
 CTATCCCTGTGAAAAGAAATAGCTGTAGTTTTTCATGAATGGGCTTTTTTCATGAATGGGCTA
 TCGTACCATGTGTTTTGTTCATCACAGTGTGTGCCCTGCAACCTAAACCAAGTGTGGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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 100211-826660

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE
 HPPQEQLALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMG
 ECSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFTITSKNMVRHLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKCRDMNEVETQFKAFLIRLLRLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTESQIEFALC
 RTQNKELQWLLDESFKGDKIKTQEFQILTILGRNPVGYPLAWQFLRKNWNKLQKFELGS
 SSIAHMVMGTTNQFSTRTRLEEVKGFFSSLKENGSQLRVCVQQTETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGGACCACCATTATGACACACGGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCGAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTGGGGCTCAAAATTCACAGAAGACCACCATCCACTCAGCCCCCTCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCGTGCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACAATCATTATCTACTACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGGAATGCCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

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FIGURE 250

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLRGGGIFSNLRVQGCMFPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC
PSC

0999728.11001

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCA
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGACGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCACAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 253

AGTGACTGCAGCCTTCTTAGATCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCTTGATCCTGCCAGACCAC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**AT**GAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGTGCTGTGAAGGAGCCACAGGAGGAGGTGG
TTCTTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCTCGCCCC
CTTCATCCCAATCAGCTTGATCCACAGGAAAGTCTTCCTTGGGAACAGAGGAGCAGAGACC
TTTA**TAA**GACTCTCTCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAACCTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTTAGAGTTCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAA
AAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTCCCGCTGCTACCGCTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGTCAGGAGTGGAGCC**ATG**AGCTGCGTCCTGGGTGGTGTTCATCCCCCTTGGGGC
 TGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAAAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCT**TAG**ACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCTGGTTGCCATGACT
 GTGAGATAAGTCAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACC GGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCAAGCTCCAGTG
 TGGAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCACGTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTTACAAAAAATC
 CAAGTTAGCCGGGATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAAGCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

FIGURE 256

MSCVLGGVPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNSHESRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLWRVSSGR
GGSRLCVLFVCFETGSHSATDAGVQWHRHRAIKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGG
GTCTGGGCTGCCCCTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTG
TGTCCTTCTTGGCCCGGGCTTTTGGGCCGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCCCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

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FIGURE 258

MSGGLPIVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTS
VTLHHARSQHHVVCNT

0909720-112001

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAAGCTTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTACCTTTTCAGTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECCLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

09030720-44004
FOUO-222666

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTTGTCATTGCTGGTTCTGTTCCTTGCAGCTTTTCTGCCCGCCGCGAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCCAAAGCAACGAGGGGCATACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCTGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACCTT
 GGCACGTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAACCAAGATCATTTACAACCTCCAGACAAAGAGAAAA
 GCTGCCCTCTGAAGTAAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCCTTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCCTTTCCCAAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACT
 GCTCCCCAGCATTACTGTAACCTTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCTAATATTTACCACCTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCATTTTCACTGCCCAACTAAAATACTATTAAATATTTCTT
 CTTTTCTTTTCTTTTTTTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC
 AGAGCTCAAGAGATCCTCCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTTCTATTGAGGTTAAACCTCTATTTCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTTTGACATCATTGAATTCTCGTTTCACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC
 TAGAAAAATACTACAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
 TGTTACCTACTCTTATAGTCAATGCGTTCACTGTTTCAGCCTAAAAATAATAGTCTGTCCC
 TTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAATAGCCCTTCAAATGATAATTCCTCC
 AGAAAAACAGTCTAAGGGTGAGGCCCAACTCTAGCCTCTCTGTCTGTCTGCTCTGTCTGT
 TTCTCTCTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

MMVALRGASALLVFLAAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLRDEADCEIVSEDKTLAEMLL
QEAEKEKKIRTLLNASCDNMLMGIKSLKIVKMMDDTHGSMWKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAAPRKQILTLWSQGTGQVIYKGLFFHNGATSNEIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT
PCRSQDAEASFLLCGVLVYVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKOLYAWNENQIYYKLQTKRKLPLK

FIGURE 263

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTCCGAGCTCATGGGGCTGTGGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGAGGAGAGGAGCGGCCGCGCCCGCTGCCAAAAAGC
 AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTC
 GGAAGGAGAAGCCTCAACAACACAACCTCACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCTCGACGAGAGACCCGACGCA
 TGAGAGCCAACTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTTCACAGCCACCCAGAGGACTTCCTAAAAAGCACAAGGCGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAA
 CTAAGGGGCCACTCCGCGGCTGTGCACTCGTTTGGCTTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGCGGGTGCCGCGCCGTGCCGC
 CTGGCCCTCTCCCCAACGCCAGGTCTTGCCCTTGCCAGTGCCAGTAGTATTATCTCTA
 CAATACCCGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGGCTG
 TTTACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCTGA
 AGAGCCTGGGTGCCCTGAAGAAG**TG**ACTCTGGGAGGGCCCGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTCTCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTT
 AGGTCTCTCTTCTTCTGTGGCTGTGACTCCTCCTGACTAGTGGCCAAGGTGCTTTTCTTC
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAATGTGATTTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCATCACAGAAGTGTGTTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCAAGAGTGGTAAAAGTGGGAACCACTGTGCTTTGAAACCAAAA
 TTAGAAACACATTCTTGGGAAGGCAAGTTTTCTGGGACTTGATCATACATTTTTATGGT
 TGGGACTTCTCTCTCGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTTATCAAG
 TTCATCAGATATTTGAGTGCCCACTCTGTGCCCAAATAAATATGAGCTGGGGATTAAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLLALMATAAVARGWL RAGEERSGR PACQKANGFPDPKSSGSKKQK
QYQRIRKEKPPQHNFTHRL LAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTL RVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNTHAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVR AFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGH LKRASNESTRQLRQQQLTQ
AOETLKS LGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTTCCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACTCCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGCACTGATTCAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTA~~AA~~AGGCCGGCAGAAGGGAGGCACCTTGAGAA**ATG**CTCTTT
 CTCACAGGACCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCTTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTTCAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCACGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAA**TGA**T
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTATGGGATGTATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCAATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGCGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCGAACCCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCCTGGCCGAGATGCGGTAGGAGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACC CGCCACCCAGCCCATGGCGAACCCCGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGACATGTAAAAAAAAAAAAAAAAAA

270/330

FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIV
VFSLAALLLAVGLALLVRKLRKLRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

270/330

FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTC AATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTC TAAATTGGACT
TTATTAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

090973-11001
10021-02650

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRNSGSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

0999728-112001
FOOT-826860

FIGURE 273

GCCAGGAATAACTAGAGAGGAACAATCGGGTTATTTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCCCTGCTGCACCACTCAAATACCTTCTTCAATTAAGCTGAATTAATATGGCTTTGAAGATA
 TTGTCTATTGTTATAGACTCTCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAA
 TGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAACATG
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTTACAGAAATGTGGAGAGAAAGGCCAATACATTCACCTCACCCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACCACCAAGGCAAACTGTTGTGCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGTAAAG
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCAAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCGAATATGATTTCTACAAAAAATCTGTATG
 GAAAAGATTTGCAATTTCTTCTGATAAAGTACAAACAGAAAAACCATTAATCAAGAAGCTCCAAG
 CAAAGTATTGATTTCTGTTGTTGTAATTTGTAACGAAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAACATAAAGTGCATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATTT
 TTA AAAACACCATACCCATGGGTGACACACCTCTCCACCTGTCTTCTCATTGTGTAAGATC
 AGTCAAAGAATTTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAAGACCGCT
 AATTCGAATGAATCAAGCAGCAAAACATTTCTGCTGACAGCTGTTGAAAATGGATCCTGGG
 TGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAATAAAGCTAACTCCAATAAAAAAGC
 AGTGTATGAAAGAAACACACTGTCGAGGATTACCTACATCTCCTGTTGGAGGAACCTTCCAT
 CTGCTCTGGAATTAATATGCAATTTCAAGGTGATTGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTG
 AAACAAGTGGGGCCATTTGTTCAATTTTATGCTTTGGGAAGAGCTGCTGATGATGAAGCAGTAAT
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTTTTCAGATGAAGCTCAGAACAATG
 GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATGCTGATCTCTCCAGAAGTCCCTT
 CAGCTCGAAAGTAAGGATTAACACTGAATAGTAATGCTGGATGAACGACACTGTCATAAAT
 TGATAGTACAGTGGGAAAGGACAGTCTTTCTCATCATGACATGGAACAGCTGCGCTCCAGTA
 TTTCTCTCTGGGATCCCAGTGGAAACAATAATGGAATAATTTACAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCAGGAACCTGCAAGGTGGGCACTTGGGCATACAATCTTCAAGC
 CAAAGCGAACCAGAAAACTTAATTAACAGTAACTTCTCGAGCAGCAATTTCTCTGTGC
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATT
 GTTTACGCAGAAATTTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCAT
 TGAATCACAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAAATACGGGCTCCACT
 GAATAGAGCGCGTACATACCAGGCTGGGTAGTGAACGGGGAATTTGAAGCAAAACCCGCCAA
 GACCTGAATTTGATGAGGATACTCAGACCCTTGGAGGATTTAGCCGCAACAGCATCCGGA
 GGTGCAATTTGTGGTATCACAAGTCCCAAGCCTTCCCTTGCTTGACCAATACCCACAAGTCA
 AATCACAGACCTTGATGCCACAGTTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAG
 GAGATAATTTTGATGTTGGAAAAAGTTCAACGTTATATCATAGAATAAGTGCAGTAAATTTCT
 GATCTAAGAGACAGTTTGTGATGCTCTTCAAGTAAATACTAGTACTGTGTCAGCAAAAGGA
 GGCCAACTCCAAGGAAGCTTTGCAATTTAAACCAGAAAAATATCTCAGAAGAAAAATGCAACCC
 ACATATTTTATGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATGCAACATT
 GCACAAGTAACTTTGTTTATCCCTCAAGCAAAATCCTGATGACATTTGATCTTACACCTACTCC
 TACTCCTACTCCTACTCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTAT
 TGTCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTAAGTACCACATTGGAACCTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGTGTTTAAAAAACAACAAATGTGAAGT
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAACTCATAAAAATAATTT
 TTAAGATGTCGGAAGAGGATACCTTTGATTAATAAAAAACACTCATGGATATGTAAAAACTGT
 CAAGATTAAAAATTAATAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGAATGAC
 AAAGATCCTTTTTCATACTGATACCTGGTGTATATTTATTTGATGCAACAGTTTCTGAAAT
 GATATTTCAAATTCAGTCAAGAAATTAATCATCTATCTGAGTAGTCAAAATCAAGATAAA
 GGAGAGCAATAAACAACATTTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 274

MGLFRGFVFLLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGENTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSTRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDBGVYSRYFTAYTENGRYSLKVRAHG
 GANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLATVHEDKIIILTWAPGDNFVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSANIAQVTLFIP
 QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCG
GGCAGGGGTGACACAGGTGTATCTTTTGTATCTCGTGTGGCTGCCTTCTTATTTCAAGGAAAG
ACGCCAAGGTAAATTTGACCCAGAGGAGCAATGATGTAGCCACTCTTAACCTTCCCTTCTTGAACC
CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAGCGCTCCTTCGGCTTTAACTT
GTGGTTGGAGGAGAAACCTTTGTGGGGTGCCTTCTTAGCAGTGTCTCAAGAGTCACTTCCGTA
GGGTGGACCAGAAAGAAAGGATGCTCCCTCTTGCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
AATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAA
GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAATCTGTTCTAGAAGGAAATGGATG
CAAGCAGCTCCGGGGGCCCAACAGCATGCTTCTGTGGTCTAGCCCCAGGGAAGCCCTCCGTTGGGG
GCCCGGGCTTTGAGGGATGCAACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTTCCGC
GGGGGCTGCTTGGCTGGATTTCCCGGGTGGTGGTTTGGCTGGTGCCTCTGCTGTGCTATCTCTGT
CCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAAACAGC
CCCACGGGGAAGGAGGGGTACAGGGCGTCTCTCAGGAGTGGGAGGAGCAGCACCAGCACTACGTGA
GCAGCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGTGCAGGAGAGGAGTGAGCGCTCAGGAA
TGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAAACCCAG
GCCGACCTCTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG
CCACAGAGATGACGAGCGCTTTTCGATAGCTTTACTCTACAGAGAGGTGTACAGGCTGGAGAGTGG
CCTTACCCGCCACCCGAGGAGAAGCCTGTGAGGAAGGACAAAGGGGATGTGTTGGTGAAGCCATT
GAATCAGCCTTGGAGACCTTGAACAATCTGACAGAAACAGCCCCAATACCCGTCTTCACCGGCCCT
CTGATTTTCATAGAAGGATCTACCGAACAAGAAAGGACAAAGGGGACATTGTATGAGTCACTCTCAA
AGGGGACCACAAACAGCAATTCAAACGGCTCATCTTATTTGACACCTTACGCCCCATCATGAAAGTG
AAAAATGAAAAGCTCAACATGCCCCAACACGCTTATCAATGTTATCTGCTGCTCTAGCAAAAAGGGTGG
ACAAGTTCGGCAGTTTCATGCAGAAATTCAGGGAGATGTGCTATGAGCAGGATGGGAGAGTCCATCT
CACTGTGTTTACTTTGGGAAAGAAATAAATGAAGTCAAGGAATACCTTGAAACACTTGCAAA
GCTGCCAATCTCAGGAACCTTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGAGCTTG
ATGTTGGAGCCCGTCTTGGAAAGGGAAGCAACGCTCTCTCTTTTCTGTGATGTGGACATCTACTT
CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAGGATTTTATCCAGTT
CTTTTCAGTCAGTACAATCTCTGGCAATAATACAGGCCACCATGATGACGTCCCTCCCTTGGAAACG
AGCTGGTCTAAAGAAGGAAATCTGGATTTTGGAGAGACTTTGGATTGGGATGACGTTCAATATCG
GTCAGACTTCATCAATATAGGTGGGTTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
CTTTTCTCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACCTCTTCCACC
TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCATGCAGTCCAA
GGCCATGAACCGAGCACTCCACGGCCAGCTGGGCATGCTGGTGTTCAGGACGAGATAGAGGCTCAC
CTTCGAAACAGGAACAAGACAAGTAGCAAAAAACATGAGACTCCCAAGGAAGGATTGTGGGAGA
CACTTTTCTTCTTCTTTTCAATTACTGAAAGTGGCTGCAACAGAGAAGAAAGACTCCATAAAGGACG
ACAAAGAAATTTGGACTGATGGGTCAAGATGAGAAGCCTCCGATTTCTCTGTGGGCTTTTTC
AACAGAAATCAAAATCTCCGCTTTCCCTGCAAAAGTAAACCAGTTGACCCCTGTGAAGTGTCTGACA
AAGGCAGATGCTTGTGAGATTATAGCCCTAATGCTGTGGAGTGTGATGCTTTTACAATACACT
GAGACCTGTGTTTGTGTGCTCCTTTTAACTGTCTCCGCTTTTTTCTTTTATTTAAAAAT
TAGCATGAAAAGGCAGCATATTTCTCCTCATATGAATGAGCCTCAGCAGGCTCTAGTTTCTCAT
AATGCTAAAAATATCAGAAGCGAGGAGAGGAGATAGGCTTATATGATACACTAGTGAGTACATTAAGTA
AAATAAAATGGACAGAAAAGAAAGAAACCAATAATTCGTTCTATATTTCCCAAGGATTAACCA
AAAAATAATCTGCTTCTTTTGGTGTCTTTTAACTGTCTCCGCTTTTTTCTTTTATTTAAAAAT
GCACCTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCATTTCGAAGCCTTACAAGAGA
GCACAAGTTGGCCTTACATTTTATATTTTAAAGAGATCTTTTGTAGATCATTTAGAACTTTTCA
GTTCAAAGCATCAATTTGATGCCATATCCAAGGACATGCCAAATGCTGATTTCTGACGAGCTGAAT
GTCAGGCATTGAGCATAGGGAAGGAATGGTTTGTACTAATACAGAGCTACAGATACTTTCTCTGAA
GAGTATTTTGAAGAGGAGCACTGAACACTGGAGGAAAAAGAAATGACACTTCTGCTTTACAGAA
AAGGAAACTCATTCAGACTGGTGATATCGTGAATGACCTAAAGTACAGAAACCAATTTCTCTCA
GAAGTAGGGACCGGTTTCTTACCTGTTTAAATAAACCAAGATATACCGTGTGAACCAACATCTCT
TTTCAAACAGGGTGTCTCCTCTGCTGCTTCTGGCTTCCATAAGAGAAATGGAGAAAATATATATAT
ATATATATATATTTGAAAGATCAATCCATCTGCCAGATCTAGTGGGATGGAAGTTTCTGCTCATCA
GTTATCCACCCAGGCGAGGTGGAAGTAACTGAATTTATTTTAAATTAAGCACTTCTACTCAATCA
CCAAGATGCTTCTGAAATTTGATTTTATTACCATTTCACAACTATTTTAAAAATAAATACAGTTA
ACATAGAGTGGTTTCTTCTTCACTGATGTGAAAATTTATAGCCAGCACCAGTGCATGAGCTAATATCT
CTTTGAGTCTTGTCTTCTGTTGCTCAGAGTAACTCATTTGTTTAAAGGCTTCAAGAACATTCACG
TGTGTTGTGTTAAAAATGCATTGTATGATTTGTAAGTGTAGTTTATGAAATTTTATTTAAACAC
AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

09999728.11001

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVFPDSFTLQKVYQLETGLTRHPPEKPVKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMANLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNCR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLFLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

090929-12001
10021-526660

FIGURE 277

GAAAGAATGTTGTGGTGCTCTTTTTTCTGGTGACTGCCATTATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCGTCTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTTGTAAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTAAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (n = 10) and the intervention group (n = 10). The control group received a standard 12-week program of physical education and sports. The intervention group received a 12-week program of physical education and sports, plus a 12-week program of cognitive-behavioral therapy. The subjects were assessed at baseline, 12 weeks, and 24 weeks. The dependent variables were: (a) physical fitness (VO2max, heart rate, and blood pressure), (b) psychological variables (anxiety, depression, and self-esteem), and (c) quality of life (physical and mental health).

FIGURE 278

MLWLLFFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFWFVVTDPSPKNHTLPAVEVQSAIRMKNRINNAFFLNDQTL
FLKIPSTLAPMPDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAAGCTGGGTTTCCCT**CATGT**
 ATGGCAAGAGCTCTACTCGTGC GG T GCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGTCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTGGCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCTTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCTTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCCTAAATTCAAAGTGTAAATGACATTTTTATTTTATGTCTC
 TCCTTAACATATGAGACACATCTTGTTTTACTGAATTCCTTTCAATATTCAGGTGATAGATT
 TTTGTCTG

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FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLETD

099730-12001

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCA**TCGA**AGTTCTTAGCAGTCTGGT
ACTCTTGGGAGTTTCCATCTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCTAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT**T**
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCTGTGATTTC
ATCCAACACTACTACCTTGCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDLFNGRVCP

0909720-112004
FOUO-026060

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGAACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGAAGGTCCAGCGATGGTCCGGAGTCCACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCGTGTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCCAGAAGTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGTCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCCAGGAAGTTCGGGCAAGCCTGTTGGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAACTGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

LEWIS & CLARK

MPVPALCLLWALAMVTRPASAAPMGPELAQHEELTLFLHGTLLQGLQALNGVYRTTEGRLTK
ARNSLGLYGRTIELGLQGEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVLQRLSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGCAAGTTTGTGTGACGTCAACGGAATCGCTATCTCCTTCCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATACATATGCGAGTTACCATCCC
 TAAATTAGGTCTTTCTCCAATGTGTCTCCAAGCAAGATTCATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAATAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTAACAAACCCAGTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCCCTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGTATAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTCTTTTTCATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATATGGGCAACCAATCTT
 TGGAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAAAATTGCATACGTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGAGGGGAAATGGGCTTTTGTAGAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGGAATTAAGTTTAGCTGTTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MAQQACPRAMAKNGLVICILVITLLDQTTSTHSRLKARKHSKRRVRDKDGLDKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTGEGFVDVNGIAISFLNWDRAPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTTCCCCGCGCGC
CCCGAGCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTTGCA
GCTCCGCTGCTGCTTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGGCCCCCT
CTCAATAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVGS AKPVAQPVA ALESAAEAGAGTIANPLGT LNPLKLLLS
SLGIPVNH LIEGSQKCVAELGPQAVGAVKALKALLGALT VFG



TGAAGGACTTTTCCAGGACCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
CCTTGGCCTCCGACGCCGATCACATGAAGTGGTGCCAAAGTCTCTGCTCTCCGCTCCTCG
GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
TCAGAAACCAAGACCAAGCAGGTGATGACAGGCTCCAGGGGAGAAGGAAGATGAGCAGGAG
CCAGCGAGGAGAAGCCGGTGAGGAAGAGAAAGCTGGCTGATGCCAGCAGCGACGACGATG
CCCAAGGAGATCTCAAACTTCGGATTTCAGCTGCTGCGAAAGATCTCCATGAGGCAGATG
CAACATGGCTTCTCTCCATTGGCATGTCTTGGCCATGACAGCCTGATGCTGGGGGCCA
TAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG
CCCGGGCTCTGCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCCCGCAACTGGAACT
GGGCTCTCAGCGGGGATTTTGCCTTTCATCCACAGGATTTGATGTCAAAGAGACTTTCT
TCAAATTTATCCAAGAGGATTTTGTATACAGAGTGCCTGCCATGAATTTTCGCAATGCCTCA
CAGGCCAAAGGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAAATTTCCAACT
GTTTGATGAGATTAATCTTGAACCAATTAATTAATCTTGTTGATATCATCTTTCAAAGGGA
AATGTTGACCCCATTTGACCTGTCTTCCAGGAAGTCACACTTTCCACTTGACAAGTAC
AAGACCATTAAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
TTTTCGTTGTATGCTCTCAACTGCCCTACCAAGGAATGCCACACATGCTGGTGGCTCTCA
TGGAGAAATGGGTGACCCTCGCCCTTGAAGACTACTGCACACAGATGCTGTGGAGACA
TGGCTCAGAAACATGAAACCCAGAAACATGGAAGTTTTCTTCCGAAGTTCAAGCTAGATCA
GAAGTATGATGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAGAAGATCTTCCACCTTTG
CTGACCTTAGTGAACTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGTTTTACGAAGA
ACAGTGATTGAAGTTGATGAAAGGGGCATGAGCAGTGGCAGGAATCTTGTCAGAAATTAC
TGCTTATTCATGCCCTCTGTTCATCAAAGTGACCGGCCATTTCATTTATGATCTATGAAG
AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAAG
ACATGCATAAGCACTTCGTGCTGTAGATAGTCTGAATCTGAGTATCAACACACACAGGA
TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTTAGGGTGTCTC
AAATAAATACAGATGCCCCATATCTGAGGGGGATACATCAAAGACCCCAAGCAGATGC
CTGAACCGTGCAGAGTGTCAACCTTATATATATTTTCTACACATACATACCTATGAT
AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAATAACAACATTAAAGTAAA
TGAGTTACTTGAACGCAAGCACTGCAATACCATACAGTCAAACATGATTATAGAGAAGGCTA
CTAAGTGACTCATGGCGAGGAGCATAGACATGTGGAGACATTGGGCAAGGGAGAATTCA
CAACCTGGGTGGGACAGGACAGGACATGAAGATTTCCATCCCATACTCAGAATGGCATGC
TGCTTTAAGACTTTTAGATTGTTATTCTGGAATTTCACTATTTAATGTTTTTGAGCCATGGT
TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCCATGGATAAGGGGAGGACTACTACAAA
GCATTTAAATTTGATACATATTTTTTAAAAAAGAAAAAAGAAAAA

MKVVPSSLSSVLLAQVWLVPGLAPSPQSPETAPQNQTSRVVQAPREEEDEQEASEEKAGE
 EEKAWLMASRQQLAKETSNFGFSLLRKISMRHDGNMVFSPPFGMSLAMTGLMLGATGPTETQI
 KRGLHLQALKPTKPGLLPSLFKGLRETLRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
 DTECVPMNFRNASQAKRLMNHYINKETRGIKPKLFEINPETKILIVDYILFKGKWLTPFDP
 VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
 ALEDYLTDDLVTWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIFSPFADLSLSA
 TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDPRPFHMIYEETSGMLLF
 LGRVNVPTLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTGTTCCC
TGTCAGAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCCAGTAGGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGGCCAGG
CTGTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVPKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCTGCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTC
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGCCAGCGTGCATGAGAATGACAAG
CGTGCGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTTCTGTTTTGATTGGAGTGGAATATGGAACCTCATGTTGGTTA
CAGCAGCAGCCGTGAGATAAAGTGGGACAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
 GVIYQTFCDMTSGGGGWTIVASVHENDMRGKCTVGDWSSQQGSKADYPEGDNWANYNTFG
 SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
 YQKYPVKYGEKGCTWDNPGVIPVYDFGDAQKTASYSPYQGQREFTAGFVQFRVFNNERAAN
 ALCAGMRVTGCNTEHHICGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
 FYR

CGCGAGCCGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCGCCACCTCGGCTGGGAGCC
CACGAGGCTGCCGCATCTTGCCTCGGAAACA**ATG**GGAATCTGGCGCGCAGGTGCTTGGGCCG
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCG
ATGGCGGCATCTGCAAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
AGAGACTCTCCAACATGTGCCTTTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCCACCACATGAAACCTACAGCG
GCATCTAATAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACTATGCAT
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
CTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGGAAATCCATGGACCAAGGATGGA
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAAATATCTCT
CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCCATCTTTTTTTTTTTGGCT
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
CAGAAATTATACAATCAAACCTAGATCTGAAGCATTAATTTAAGAAAAACATCAACATTTTTTG
TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVP
SDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSV
SQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSI
LYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**ATG**GCGACCCGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCTGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAATTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATCTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAG**CTAA**TTGGGAATTGAATTCAAGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAAGTACTGCTGGGTTTGTGCGGTTTCATTTTAATACCTTGTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAAACCTGGAAGCAAAAACCTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAAGTCTTTACCTGGAACA
 AGCACTCTCTTTTTTACCACATAGTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACCTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCCTGACTGTATTATCTGGGTATCTGCTGTGCTGCACTTCATGGTAAACGGGAT
 CTAAAATGCCTGGTGGCTTTTCACAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCTATGTCTCTTTTGAATGTAAACAATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLALLAQLSDAAKNFEDVRCKCICPPYKENS
GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILG
LLLLLYMVYLT
LVEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLA
RSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVLS

U9973-4204

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCA**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTGCTGCTGCTGCCCAAGGCCTTCTGTCCC GCGGGAAGCGG
CAGGAGCCGCCGCCGACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTCGAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCTG
ATGGGGCAGATTATTCGAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGTAAGTAGAATCATCCTAATCATATTACATCAAT**TGA**AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTAGTTTACATAAGAATG
TTTACTCAATGTTTTAAGTGTTTTGCCCCAAAATTCACTAACAAGGCAGAAGTCTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILLI
ILHQ

000072241004
000072241004

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCATGTTTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTTCAAGAT
AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC CGGTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAAACACGTGACCAAGGTAGAAATGGATATTTTCAGAGACGGCGCGCAAAGGA
GGAGATTGTATTTCTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTTCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACGGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACCACTCACTTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCCTGTGTGTGCTCTGGGCCACTCTACAGTGATTTTCAGACTCCCGCTCTC
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCTCCTGTGGGCAGGGTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

0000724000
0000724000

FIGURE 305

CTATGAAGAAGCTTCTCTGGAACAATAAGCAAAGGAAAAAACAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGG
ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGCTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAACCATTTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTCGGGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCTGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACTCATCCCTGTGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTGTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGAGTCCTTACCCAAAAGTTCAAATTTGTGTCAGTGACATTTACCAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCDKNKLNVFSRVKLFGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSSEFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGG
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
CAACCTGGATATTCTGAGACATATTTTGGGGGATTTTCACTGAAAAAAGTGGGGGATCCCT
CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGTTGGGTTCCTTCTGACATTGGCAGTG
CCCCAGTAGGGGTGGGATGAGCGAATATTTCCAAAGCTAAAGTCCACACCCTGTAGATTA
AAGAGTGGATTGTGCAGGAGTGTGCCCCAAATACAGTGGAAAGTGCCTGAAGATATTTAA
ACCACGTCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGGGACAGACACTG
GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACCTGGCTGCT
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCTCAGTCTCTGTGGGTGGGGCAG
CGAGTCGGGGCCTGAGCGCTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGCGCT**ATG**CGGGCGCTGGC
CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCG
CGCAGCGGCGGTGTGTCCCGCGGCACCAAGTCCCTTTGCGAGAAGCAGCTCCTCATCCTG
CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGCCGACCGCGGCCCGAGCCTCA
GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTTCAACCCACTTCAACCTGATCCCT
GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
TTGAGAAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA
GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG
GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVPGGSRPVSAQRRVCPRGTKSLCQKQLLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

310/330

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGGAGCAGCACTG
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTTACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGCAAGCTATGAAAGGGAAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACATAG

FIGURE 312

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
```

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKQAREQHWDPRPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRRL
RQDPQLKGI VTRLYCRQGYLQMHPD GALTGDKDDSTNSTL FNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLPSELFTPECKFKESVFENYVIYSSMLYRQESGRAWFLGLNKEGQAMKGNR
VKKT KPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSKT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAT
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAATGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AAATAAACAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCAATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAAGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAAGTGGTGTGGTGGTGGTCTTTCTTTCTTTTGAATTTCCACAAAGAGGAGAGGAATTAATAATACATCTGC
 AAAGAAATTTAGAGAAGAAAAGTTGACCCGCGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTTGTGCTATGTTGACTAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAAACACCTGGATTTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATCAACTGTTTGAATTCAGAAGGACCAACACCAGATAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAACAACAGTTTCAAGAGGTGATTGTTGTTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG
 GCACCTTGAAGTCTCAGAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTCAATGGTCTGGCGA
 AGCTCAACACTCTGGAACCTTTGACAACTGCTCTTACTACCATCCGGAATGGAGCTTTTGTATACTTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT
 GCGCCGACTAGACTTAGGGGAATTTGAAAAGACTTTTATACATCTCAGAAGGTGCTTTGAAGGTCTGTCCAAC
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACAACGCTCATAAAACCTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGATGCACCTTCAAAAAC
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGCCATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCGCTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTAAATTTCAAAATGTAAGTGTGCAAGATA
 CAGGCGATGTACACATGTATGGTGAGTAATCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACGCTCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGTCCCACTCCAGTGCTGACTGGGAGACCAACAAATGTGACCACTCTCTCACAC
 CACAGACACAAGGTCGACAGAGAAAACCTTCACCATCCCACTGACTGATATAAAGCAAGTGGGATCCCGGAAT
 GATGAGGTGATGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCCATGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCTATAAAATCTCCCTTCAACCACACAACAACAGTTTAAACAATAAATCAATACA
 CAGTTCACTGATGAACCGTTATTGATCCGAATGAACCTCTAAAGACAATGTACAAGAGACTCAAATCTAAACA
 TTTACAGAGTTACAAAAAACAAACATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPELLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NINTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVSGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTKFTFTIPVDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
 HHAPTRTVEIINVDDEITGDTPMESHLPMPIAEHEHLNHYSYKSPFNHTTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGTGTCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCTGTCGGA
 GCGCGCCCGCCCGCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATC
 GGGATGTCCTCTCCTTCTCCTCTTGCTAGTTTCTACTATGTGTGGAACCTTGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACTCTGGATATGTAATGGCTGCTCACCAGATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTCTCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCAAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCACTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCACCTGGACGAGTTCTGCTGCAGAACTTACCATGTCTTACTCTGGACTGTA
 CCAGTGACACGACAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAAGGAGCAGTGACAGGACTAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCGAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
 CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCCCGAGCCAGAGCAGAGCCCTTCCAA
 ACGGTCGAAATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGCACGGAACAGATTAGATGAGCATTTCCTTATACAATAACAAACAAAGCAAA
 AGGATGTAAGCTGATTCTCTGTAAAAAGGCATCTTATGTGCCCTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTGACCAGGACCTGTGGTGAGAAAGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATT
 TTCAAGAGGAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATTGAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTCTCATAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTGATTGAGCCCAAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATAATGGAGCAATTGTGGATTTCCTCAAAAT
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCATT
 TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCCACATACCATTATAGTCTCTTCTTCTGAGAAAAATGTGAACAGAAATGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCCTGGGTGACAGAGCGGACTCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFAQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 316

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCCGCGCCACGGCAGCGGACGCCA
 CCATGGCGCTCTGCTGTGCTTCTGCTCTCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGAGTATCACTACT
 CCTCGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCTGCCATTGCAAAATTTAGCGTTAGTCCCGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGTGGATCAAGTGATTTTTTAT
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAGGCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGATGCATCAATAAATGTAACGAATTTACAACGTGCAGATATTGGCACATATCAGTGCAAAAGTGAA
 AAAAGCTCCTGGTGTGCAATAAAGAAGATTCATCTGGTAGTCTCTGTTAAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACCTCCATTACAG
 TATGAGTGGCAAAAATTTGCTGACTCACAGAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAATGCCTCTCTGAGTACTCTGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCCTGTTGCGCTAAACGTTGTCCTCTCAAATAAAGCTGGACTAATTCAGGAGCCATTATAGGAAT
 TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTTGTCTGCTGTAAGAGCGCAGAGAAAGAAAATGAAAA
 GGAAGTTTATCAGCATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCCTGCCAGAGCTACATCG
 CGAGTAATCATTCATCCCTGGGGTCCATGTCTCCTTCCAACATGGAGGATATTCGAAGACTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCCTTACAA
 GACTGATGGAATTTACAGTTGTATTAATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTGAAGACAC
 ATCTACTTTATGCAATGGCATTAGACATGTGAAGTCAGATGTCTATGTCAAAATTAGTACGAGCCAAATCTTTGT
 TAAAAACCCCTATGATAGTGACACTGATAGTTAAAGATGTTTTATTATATTTTCAATACTACCCTAACAA
 ATTTTTAACTTTTCATATGCATATTTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAATTTCTTACGTTCTGTTTAAATGTTTTTGTCTATTAGTTAAATACATTGAAGGGAATACCCG
 TTCTTTTCCCTTTTATGCACACAACAGAAACACGCGTTGTCTGCTCAAACTATTTTATTGTCACCTACA
 TGATTTACACAATTTCTTAAACAACGACATAAAATAGATTTCCCTGTATATAAAATACTTACATACGCTCCA
 TAAAGTAAATTTCTCAAAGGTGCTAGAACAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATATTAAGAACTTAGGCACTTGACTAACTTTAATAAAATTTCTCAAACCTA
 TATCAATATCTAAGTGCATATATTTTAAAGAAAGATTATCTCAATACTTCTATAAAAAATAAGTTTGATGG
 TTTGGCCCATCTAACTTCACTACTATTAGTAAGAACTTTAACTTTAATGTGTAGTAAGGTTTATTTCTACCTT
 TTTCTCAACATGACACCAACACAATCAAAACGAAGTTAGTGAGGTGCTAACATGTGAGGATTATCCAGTGTAT
 TCCGGTCAATGCATTCCAGGAGGAGGTACCCATGTCACTGGAATTTGGGCGATATGTTTTATTTTTCTCCCT
 TGATTTGGATAACCAATGGGAACAGGAGGATAGTGATTTCTGATGGCCATCTCCCTGCATACATCTCTGGCTT
 TTTCTGGGCAAGGGTGCCACATTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT
 TAAGTTAATTTCAAAGGAAAAATCATCATCTATGTCCAGATTTCTCATTAAAGACAAAGTTACCCACAACAT
 GAGATCACATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAACCACTCATGTGTAATAGGCGTATAA
 TGTATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAACTCAACACAGTACTTCTTAAACAA
 CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCTTGAAGGACATGCTGTTTTAGTCCAGTGTTTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCTT
 AGCAAACTAATGCAGAAACAGAAAATCACTACCGCATGTTCTCACTTATAAGTGGGAGGTATGATAAGAACT
 TATGAACACAAAGAAGGAAACAAATAGACATTGGAGTCTATTGAGAGGGGAGGTTGGGAGAAGGAAAGGAGCA
 GAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGATGAAATAATATGTACACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAAACCTTCATGTGTATCCCTAAACCTAAATAAAAGTTAAAAAATAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFARSL SITTP EEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARC YVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGS DQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLII FCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTFPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

FIGURE 320

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
```

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><subunit 1 of 1, 206 aa, 1 stop
```

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARFPCPLLATASQMOMVVLPCLGFTLLLSQVSGAQGGQEFHFGPCQVK
 GVVPPQLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLVHTLLEFYLKTVFKNH
 HNRTVEVRTLKSFSSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRLFRRAFKQLDVEAAL
 TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACACGGTCTCAGGAGATGCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAATCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACCTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

000075-11004

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACCGGGCTACAATTAATACATAACCTTATGTATCATACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGCATGTTGGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCCTCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTGC
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACTGCGATGACAACGGACGACACAGAAG
 TGCCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTTCAGACCATCACAGGCAGTGATCCCAGGAAGCCATCTTTGACACCCCTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
 GTCACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT
 GGTCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACCACATCACTGAGGTACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCAAGAGTCACTGACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACG**TG**AGTGCAAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCCAGCCACGCGCCTCACTTCCAGGTCTCTTACTGCGTGTGAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCCTAGCCGTG
 GGCCCCACCCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
 TTAAATTCAGTGTGGCCAAAAAAA

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLPAGHAALETQTL
ETSSRASTPAGPIPEAETRGAKRISPARETRSFKTSPNFMVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAFDTLCTDDSSSEAKTLTMDILTLAHTSTEAKGLSSESSASSDGHPV
ITPSRASESSASSDGHPVITPSRASESSASSDGHPVITPSWSPGSDVTLLEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEPTSY
VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAAKNFTPSETPTMDIATKGFPFPTS
RDLPSVPPTTTNSSRGNTSLAKITTSAKTMTKPPQPRPRLPGRGRPQT

amino acids 252-256, 445-449, 451-455

amino acids 84-90

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
404-408, 414-418, 431-435

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-320, 349-355, 386-392, 397-403, 449-455

amino acids 385-393

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGCGGATTGCGCCGGTCTCTCCGCGG
GCGCGACAGAGCTGTCTCGCACCTGGATTGGCAGCAGGGGGCGCCGGGTCTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCGACGCTTCTTAAAGCAAACATAAGAACGAGGGAGGATTAT
CCTTGACCTTTGAAGACCAAAACATAAACGTAAATTTAAATGTTCTTCTGGGGGAGAGGGGAG
CTTGACCTTACACTTTGGTAATAAATTTGCTTCTGACACTAAGGCTGTCTGCTAGGGAAT
GCCTCAAAAAGAGTCTAGAAGATGTGTCATTGACATCCAGTCATCTCTTTCTAAGCAATC
AGAGGCAATGAGCCGTATATACCTTACCTCAAGAGAGATGCATTAATCTTGTCTGTTCAA
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCCCACTGCTACCTATTTTTCTGTGCCAACGGAAGAGCTGTCCATTGAAACACGCA
AAAGGACTTTATGAGTTACAGGATAAATACAGATTTTCCATCTTTGACCAAAATTTGCCAA
CCAAGAGTTACCCCGAGGAATCTCTCTTACATGGCCAAATTTTACAAAGCAGTCACTCCCC
TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGACACAGCTTTCT
CAGAAGTTTGGATCTCAGATCACTTGGAGAAACTATTTAAGATGGATGAAGCAAGTCCCC
GCTCCTTGCTTTATAAGGAAAAAGGCCATCTCAGAGTTCAAAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCTGAAAATGTGAGTGCCTCCGACGTACGGTGGCAGTTGCTTCTCCCA
CATACACCTCGGCTACTCAAAGCCCGCCACCTTTCTACCCCAACATGCTTCAGTGACACC
TTCCTGGAGTTTCCGACCCAGCACTGGCCACCAAGCTCACCCTGAACCACTGTCACTTCTC
AGCCTCCACGACCTCATTTTCTACAGTTTTTACACGGGCTCGGCTACACTCAAGCAAT
GCTACAAACAGAGTTTCTGACTACCACTTACGAGCACTACGAGTCAAGAAAGCAGCTTAGA
AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGAATGTGTATAACCCCTA
CTGCATCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCGAGAAATCAGTACGGCTCTCC
ATTTGAAAAATGGCTTCTTATCGGTCCTGCTCTTTGGTGTCTTGTCTGTTGATAGGCC
TCGTCCTCTCGGTAGAAATCTTCCGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGACACTTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
TAGTAAACGAGAGCCCAATGCAATGAGTTTCTGCTGACTGTGCTAGTCTTAGCAGGAGTTG
TATTTTGAAGACAGGAAATGCCCTTCTGCTTCTCTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCAGCAACCTCCGCTCTC
CTGGGTTCAAGCGATTTCTCTGCCCTCAGCCTCCTTAAGTATCTGGGATACAGGCATGTGCCA
CCACACTCGGGTGAATTTTGTATTTTATGATAGAGCAGGGGTTCCACATGTGTGTCAGGCT
GTCTCAAACCTCTGACCTAGTGATCCACCCTCTCGGCCCTCCAAAGTGTGGGATACAGG
CATGAGCCACACAGAGCTGGCCCCCTCTGTTTATGTTTGGTTTTTGAAGAAGGAATGAAGT
GGAACCAAAATAGGTAATTTTGGGTAATCTGTCTCTAAATATAGCTAAAAACAAAGCTCT
TGTAAAGATATAAAGTATAATTTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATCACATCTTGTTTCAGATAAAATCAAC
TGTTTATATCAATTTCAATGATTGTTCTTTCTTTTATAGGATCTCTTAAACCTTAT
CGGATCTAGTTCTCTTCCAAATAAATTTTGAATAAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGI RGNP VYTSTQED
CINSCCSTKNISGDKACNLMI FDRKTARQ PNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVT PLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTT SATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVT SQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFKEWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSR LDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACGGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGGAAGAAGGCCAGGAGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGCAGCGGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTGTTCGTCTTCCAGGACCCTGCTGTCTCCCTCCCCTTCTCCAC
 CTCCAGCCTCTGGCTACAACACGCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTGCCAGGGAATCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCAGCTCTCTCTCTGCAGGAGCTCCGCCCCCCCATGTCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTGAGC
 CGCAGGCTGATCGCCTTCTGCAGCCACTGTCTCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAAGGAAGCC
 CCTTCCCAGGCCCCGTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGGATTCGCCGAAAGCTTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCAGGCTCTCTCTGTCATGTTCCA
 GCCTGACCTAGAAGCGTTTTCTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTGATGCCAGTGTGCGACCTGCCTTCTCCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCAGGCTCTCTGTCATCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCGACTTGAGTTTGAAGGCGAGTGGGCGCTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTGTGCATTTGGGCTGTGAGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCAGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCTTCTTGTCTGGAAAGGGTTACTTGCCTATGGGTCTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTCCAGCTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGAAGTA
 GCACAACCTACTATTTTTTTTCTTTTCCATTATTATTGTTTTTAAAGACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCCCTCTGGGTTCAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCTGCTTCACTTCCCAAATTGCGGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCCATTTCCTTTAAAAAGTGAAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAAG
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 TATTTTCGTTTTGTTGTACTTCTTCCACTCTTTTCTTCTTACATAAATTGCGGGTGTCTT
 TTTACAGAGCAATTATCTTGATATACAACCTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATCCAGCACTTCTCTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPD E SLLISLFV
FPGPCCPPSPSPFTQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQCKTGAEAPPLPG
TSQYGHERTSQYTGTS PHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE E KEAPSQAPEGD
VISM PPLHTSEEE LGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128